

GenCore version 5.1.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2006, 09:56:51 ; Search time 91 Seconds  
(without alignments)  
4194.405 Million cell updates/sec

Title: US-10-635-977-2

Perfect score: 541

Sequence: 1 MASSILKVVVSHQSCSRSSR.....LRGLKTABGALRPPPGRGKS 541

Scoring table:

OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

UniProt\_05.80.\*

1: uniprot\_eprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	390	72.1	747	Q5JZ84_HUMAN	Q5JZ84 homo sapien
2	49	9.1	518	Q8COV2_MOUSE	Q8COV2 mus musculus
3	49	9.1	781	Q8CON7_MOUSE	Q8CON7 mus musculus
4	18	3.3	375	Q4V8C1_RAT	Q4V8C1 rattus norv
5	13	2.4	101	Q96GG8_HUMAN	Q96GG8 homo sapien
6	13	2.4	261	Q58CT2_BOVIN	Q58CT2 bos taurus
7	13	2.4	266	Q922T0_MOUSE	Q922T0 mus musculus
8	13	2.4	352	TTLI3_HUMAN	Q9Y4I7 homo sapien
9	13	2.4	352	Q6AWA3_HUMAN	Q6AWA3 homo sapien
10	13	2.4	352	Q4KMS8_HUMAN	Q4KMS8 homo sapien
11	13	2.4	434	Q8NDN8_HUMAN	Q8NDN8 homo sapien
12	13	2.4	534	Q4RYO8_TETNG	Q4RYO8 tetraodon n
13	13	2.4	704	Q8BV51_MOUSE	Q8BV51 mus musculus
14	13	2.4	744	Q9H876_HUMAN	Q9H876 homo sapien
15	12	2.2	572	Q70156_ANOGA	Q7Q156 anopheles g
16	10	1.8	281	Q6ZU95_HUMAN	Q6ZU95 homo sapien
17	10	1.8	992	Q9VM91_DROME	Q9VM91 drosophila
18	9	1.7	228	Q8GQ93_PSEAE	Q8GQ93 pseudomonas
19	9	1.7	304	Q9KW29_XANOR	Q9KW29 xanthomonas
20	9	1.7	304	Q9LBJ4_XANOR	Q9LBJ4 xanthomonas
21	9	1.7	334	Q5H6T4_XANOR	Q5H6T4 xanthomonas
22	9	1.7	376	Q4HQ33_CAMUP	Q4HQ33 campylobact
23	9	1.7	502	Q688G5_ORYSA	Q688G5 oryza sativ
24	9	1.7	547	1 MCPC_SALTY	Q02755 salmonella
25	9	1.7	547	Q57IQ0_SALCH	Q57IQ0 salmonella
26	9	1.7	547	Q8Z256_SALTI	Q8Z256 salmonella
27	9	1.7	547	Q5RJM7_SALPA	Q5RJM7 salmonella
28	9	1.7	1147	Q4P5Z9_USTMA	Q4P5Z9 ustilago ma
29	8	1.5	110	Q9PCC1_XYLFA	Q9PCC1 xyella fas
30	8	1.5	119	Q5NAM5_ORYSA	Q5NAM5 oryza sativ
31	8	1.5	158	Q4IT38_AZOVI	Q4IT38 azotobacter

#### RESULT 1

Q5JZ84\_HUMAN PRELIMINARY; PRT; 747 AA.  
AC Q5JZ84;  
DT 10-MAY-2005 (Tremblrel. 30, Created)  
DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)  
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)  
DE OTTHUMP0000028514 (Fragment).  
GN ORFNames=RP3-355C18.2-002;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]\_TaxID=9606;  
RP NUCLEOTIDE SEQUENCE.  
RA Cobley V.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL022327; CAI42686.1; -; Genomic DNA.  
DR GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA.  
DR GO; GO:0006464; P:protein modification; IEA.  
DR InterPro; IPR004344; Tub\_tyr\_lygase.  
DR Pfam; PF03133; TTL; 1.  
DR NON\_TER 1.  
SQ SEQUENCE 747 AA; 83854 MW; F90948E159BBE589 CRC64;

Query Match 72.1%; Score 390; DB 2; Length 747;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 152 DIVCMDRVVEEILELAADHPILSRDNKVVQKYIETPLIICDTKFDIRQWFLVTDWNLPTI 211  
Db 358 DIVCMDRVVEEILELAADHPILSRDNKVVQKYIETPLIICDTKFDIRQWFLVTDWNLPTI 417  
Qy 212 WFKYESYLRFSFSTQPSLKLDSAIHLCCNNAVQKYLKNDVGRSPLLPAAHNMWTSFQEVYL 271  
Db 418 WFKYESYLRFSFSTQPSLKLDSAIHLCCNNAVQKYLKNDVGRSPLLPAAHNMWTSFQEVYL 477  
Qy 272 QROGRGAVGWSVIYPSMKKAIAHAMKVQADHVEPRKNSFELYGADPVLGRDPRPMLIEN 331  
Db 478 QROGRGAVGWSVIYPSMKKAIAHAMKVQADHVEPRKNSFELYGADPVLGRDPRPMLIEN 537  
Qy 332 SSPTMHPSTPTVAQLCAQVQEDTIKVAVDRSICDIGNFELLMRQPVVVEPPFSGSDLCVAG 391  
Db 538 SSPTMHPSTPTVAQLCAQVQEDTIKVAVDRSICDIGNFELLMRQPVVVEPPFSGSDLCVAG 597  
Qy 392 VSVRRARQVLPVNCNLKASASLLDAQPLKARGSPAMPDPAQPPSPALORDLGLKEEKG 451  
Db 598 VSVRRARQVLPVNCNLKASASLLDAQPLKARGSPAMPDPAQPPSPALORDLGLKEEKG 657  
Qy 452 PLALILAPLRGAESGGAQPTTKAAGVELPACPCRHVDISOAPNTGVPVPAQPAKSWDPN 511  
Db 658 PLALILAPLRGAESGGAQPTTKAAGVELPACPCRHVDISOAPNTGVPVPAQPAKSWDPN 717

```

QY 512 QLNHAHLEPVLRLGKTAEGALRPPPGKGS 541
DB 718 QLNHAHLEPVLRLGKTAEGALRPPPGKGS 747

RESULT 2
Q8CV02_MOUSE
ID Q8CV02_MOUSE PRELIMINARY; PRT; 518 AA.
AC Q8CV02;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4930524K07 product:hypothetical tubulin-tyrosine ligase
DE containing protein, full insert sequence.
GN Names:1700019P01Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
DE "High-efficiency full-length cDNA cloning.";
RN Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo S., Nikaide I., Pesole G., Quackenbush J.,
RA Schram L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

```

```

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Katsunai T., Teshiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK029745; BAC26595.1; -; mRNA.
DR Ensembl; ENSMUSG00000022388; Mus musculus.
DR MGI; MGI:1922902; 1700019P01Rik.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA.
DR GO; GO:0006464; P:protein modification; IEA.
DR InterPro; IPR004344; Tub_tyr_ligase.
DR Pfam; PF03133; TTL; 1.
DR Hypothetical protein; Ligase.
SQ SEQUENCE 518 AA; 59319 MW; 540C045659FAC0D6 CRC64;
Query Match 9.1%; Score 49; DB 2; Length 518;
Best Local Similarity 100.0%; Pred. No. 9.1e-42; Indels 0; Gaps 0;
Matches 49; Conservative 0; Mismatches 0;
QY 192 DTKFDIRQWFLVTDNPLTIWFYKSYLRFSTQRFSLDKLDSAIHLCNN 240
DB 248 DTKFDIRQWFLVTDNPLTIWFYKSYLRFSTQRFSLDKLDSAIHLCNN 296

RESULT 3
Q8CON7_MOUSE
ID Q8CON7_MOUSE PRELIMINARY; PRT; 781 AA.
AC Q8CON7;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4933401B17 product:hypothetical tubulin-tyrosine ligase
DE containing protein, full insert sequence.
GN Name:1700019P01Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
DE "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

```

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gofobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.,  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes."  
RL Genome Res. 10:1617-1630(2000).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
RA Yumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohata E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer."  
RL Genome Res. 10:1757-1771(2000).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Inotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AK030151; BAC26811.1; -; mRNA.  
DR Ensembl; ENSMUSG00000022388; Mus musculus.  
DR MGI; MGI:1922902; 1700019p01Rik.  
DR GO; GO:0016874; F.ligase activity; IEA.  
DR GO; GO:0004835; F.tubulin-tyrosine ligase activity; IEA.  
DR GO; GO:0008464; P.protein modification; IEA.  
DR InterPro; IPR002276; GPCR\_Rhodpsn.  
DR InterPro; IPR004344; Tub\_tyr\_ligase.

DR Pfam; PF03133; TTL; 1.  
DR PROSITE; PS00237; G.PROTEIN RECEPTOR\_F1\_1; UNKNOWN 1.  
KW Hypothetical protein; Ligase.  
SQ SEQUENCE 781 AA; 89398 MW; 9E98793C3351C3DE CRC64;  
  
Query Match 9.1%; Score 49; DB 2; Length 781;  
Best Local Similarity 100.0%; Pred. No. 1.3e-41;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 192 DTKFDIOWELVTDWNPITWFKESYLRSTQRFSLDKLSAIHLN 240  
|||||  
DB 395 DTKFDIOWELVTDWNPITWFKESYLRSTQRFSLDKLSAIHLN 443  
|||||  
  
RESULT 4  
Q4V8C1 RAT PRELIMINARY; PRT; 375 AA.  
ID Q4V8C1 RAT PRELIMINARY;  
AC Q4V8C1;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DE RGD1306462 Predicted protein.  
GN Name=RGD1306462\_predicted;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Testis;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Testis;  
RG NIH MGC Project;  
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BC097453; AAH97453.1; -; mRNA.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR PROSITE; PS00237; G.PROTEIN RECEPTOR\_F1\_1; UNKNOWN 1.  
SQ SEQUENCE 375 AA; 42908 MW; 566FBA119C61BE1F CRC64;  
  
Query Match 3.3%; Score 18; DB 2; Length 375;  
Best Local Similarity 100.0%; Pred. No. 2.4e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 59 ACKVCQAYLGQLEHEDID 76  
|||||  
DB 260 ACKVCQAYLGQLEHEDID 277  
|||||  
  
RESULT 5  
Q96GG8\_HUMAN

```

ID Q96GG8_HUMAN PRELIMINARY; PRT; 101 AA.
AC Q96GG8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TTL3 protein.
GN Name=TTL3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX Strausberg R.;
RA Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL: BC009479; AA09479.1; -; mRNA.
DR GO: GO:0004835; F:cubulin-tyrosine ligase activity; IEA.
DR GO: GO:0006464; P:protein modification; IEA.
DR InterPro: IPR004344; Tub_tyr_lygase.
DR Pfam: PF03133; TTL; 1.
SQ SEQUENCE 101 AA; 2054 MW; 8EACD6C1131E0DF9 CRC64;

Query Match 2.4%; Score 13; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 ROWFLVTDWNPILT 210
Db 66 ROWFLVTDWNPILT 78
|||||
|||||

RESULT 6
Q58CT2_BOVIN
ID Q58CT2_BOVIN PRELIMINARY; PRT; 261 AA.
AC Q58CT2;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Tubulin tyrosine ligase-like family, member 3.
GN Name=TTL3;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX Strausberg R.;
RA Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL: BC009479; AA09479.1; -; mRNA.
DR GO: GO:0004835; F:cubulin-tyrosine ligase activity; IEA.
DR GO: GO:0006464; P:protein modification; IEA.
DR InterPro: IPR004344; Tub_tyr_lygase.
DR Pfam: PF03133; TTL; 1.
SQ SEQUENCE 101 AA; 2054 MW; 8EACD6C1131E0DF9 CRC64;

Query Match 2.4%; Score 13; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 ROWFLVTDWNPILT 210
Db 66 ROWFLVTDWNPILT 78
|||||
|||||

RESULT 7
Q922T0_MOUSE
ID Q922T0_MOUSE PRELIMINARY; PRT; 266 AA.
AC Q922T0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 483344J24Rik protein.
GN Name=483344J24Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX NTH MGC Project;

```

```

RC TISSUE=Pooled;
RX MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101;
RA Smith T.P.L., Grosse W.M., Freking B.A., Roberts A.J., Stone R.T.,
RA Casas E., Wray J.B., White J., Cho J., Fahrenkrug S.C., Bennett G.L.,
RA Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-McKown C.G.,
RA Perlea G., Holt I., Karamycheva S., Liang F., Quackenbush J.,
RA Keele J.W.;
RT "Sequence evaluation of four pooled-tissue normalized bovine cDNA
RT libraries and construction of a gene index for cattle.";
RL Genome Res. 11:626-630(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pooled;
RX Harhay G.P., Sonstegard T.S., Van Tassel C.P., Clawson M.L.,
RA Heaton M.P., Keele J.W., Snelling W.M., Weidmann R.T., Smith T.P.L.;
RT "Sequencing and analysis of Bos taurus full-length insert cDNA
RT clones.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR ENBL: BT021865; AAX46712.1; -; mRNA.
KW Ligase.
SQ SEQUENCE 261 AA; 29911 MW; 5F069784CA162017 CRC64;

Query Match 2.4%; Score 13; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 ROWFLVTDWNPILT 210
Db 68 ROWFLVTDWNPILT 80
|||||
|||||

RESULT 7
Q922T0_MOUSE
ID Q922T0_MOUSE PRELIMINARY; PRT; 266 AA.
AC Q922T0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 483344J24Rik protein.
GN Name=483344J24Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX NTH MGC Project;

```

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC006830; AA06830.1; -; mRNA.  
 DR Ensembl; ENSMUSG0000030276; Mus musculus.  
 DR MGI; MGI:2141418; 4833441J24Rik  
 DR GO; GO:0004835; F.tubulin-tyrosine ligase activity; IEA.  
 DR GO; GO:0006464; P:protein modification; IEA.  
 DR InterPro; IPR004344; Tub\_tyr\_ligase.  
 DR Pfam; PF03133; TTL; 1.  
 SQ SEQUENCE 266 AA; 30506 MW; F8E9FB52FA8B8E98 CRC64;

Query Match 2.4%; Score 13; DB 2; Length 266;  
 Best Local Similarity 100.0%; Pred. No. 0.00031;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 ROWFLVTDWNPILT 210  
 Db 66 ROWFLVTDWNPILT 78

## RESULT 8

TTLL3 HUMAN  
 ID TTLL3 HUMAN STANDARD; PRT; 352 AA.  
 AC Q9YAF7; Q9UI99;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Tubulin tyrosine ligase-like protein 3 (HOTTLL).  
 GN Name=TTLL3; ORFNames=PRO0207;  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC The German cDNA consortium;  
 RG Tissue=Testis;  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 61-352.  
 RC Tissue=Fetal liver;  
 RA Yu Y., Zhang C., Luo L., Ouyang S., Zhang S., Li W., Wu J., Zhou S.,  
 RA Liu M., He F.;  
 RT "Functional prediction of the coding sequences of 50 new genes deduced  
 RT by analysis of cDNA clones from human fetal liver."  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: Contains 1 TTL domain.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR EMBL; AL096725; CAB46375.1; -; mRNA.  
 DR EMBL; AF078842; AAF23353.1; -; mRNA.  
 DR PIR; T12515; T12515.  
 DR Ensembl; ENSG00000156983; Homo sapiens.  
 DR HGNC; HGNC:24483; TTLL3.  
 DR InterPro; IPR004344; Tub\_tyr\_ligase.  
 DR Pfam; PF03133; TTL; 1.  
 KW Ligase; Polymorphism.  
 FT DOMAIN 1 293  
 FT VARIANT 290 290 M -> R (in dbSNP:2290305).  
 FT FTID=VAR\_020207.  
 FT I -> F (in Ref. 2).  
 FT CONFLICT 67 67  
 SQ SEQUENCE 352 AA; 40356 MW; 49FD8E8118C7C20D CRC64;

Query Match 2.4%; Score 13; DB 1; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 0.0004;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 ROWFLVTDWNPILT 210

Db 126 ROWFLVTDWNPILT 138

## RESULT 9

Q6AWA3 HUMAN  
 ID Q6AWA3 HUMAN PRELIMINARY; PRT; 352 AA.  
 AC Q6AWA3;  
 DT 25-OCT-2004 (TREMBLrel. 28, Created)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
 DE Hypothetical protein DKFZp686D076.  
 GN Name=DKFZp686D076;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC The German cDNA Consortium;  
 RG Ansorge W., Krieger S., Regiert T., Rittmueller C., Schwager B.,  
 RA Newes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;  
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX648175; CAH10554.1; -; mRNA.  
 DR GO; GO:0004835; F.tubulin-tyrosine ligase activity; IEA.  
 DR GO; GO:0006464; P:protein modification; IEA.  
 DR InterPro; IPR004344; Tub\_tyr\_ligase.  
 DR Pfam; PF03133; TTL; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 352 AA; 40257 MW; 49FD8E9CAE1CB20D CRC64;

Query Match 2.4%; Score 13; DB 2; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 0.0004;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 ROWFLVTDWNPILT 210  
 Db 126 ROWFLVTDWNPILT 138

## RESULT 10

Q4KMS8 HUMAN  
 ID Q4KMS8 HUMAN PRELIMINARY; PRT; 352 AA.  
 AC Q4KMS8;  
 DT 13-SEP-2005 (TREMBLrel. 31, Created)  
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)  
 DE Hypothetical protein (TTLL3 protein).  
 GN Name=TTLL3;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC Tissue=PCR rescued clones;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

```

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=PCR rescued clones;
RC NIH MGC Project;
RG Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC098361; AAH98361.1; -; mRNA.
DR EMBL; BC099735; AAH99735.1; -; mRNA.
KW Hypothetical protein.
SQ SEQUENCE 352 AA; 40381 MW; 49EF0C1118C7DD12 CRC64;

Query Match 2.4%; Score 13; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 ROWFLVTDWNPFLT 210
Db 126 ROWFLVTDWNPFLT 138

RESULT 11
QBNDN8 HUMAN PRELIMINARY; PRT; 434 AA.
AC QBNDN8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein DKFZp586B0320.
GN Name=DKFZp586B0320;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Uterus;
RC Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";

```

```

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=PCR rescued clones;
RG NIH MGC Project;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL833939; CAD38794.1; -; mRNA.
DR EMBL; BC098298; AAH98298.1; -; mRNA.
DR GO; GO:0004835; F.tubulin-tyrosine ligase activity; IEA.
DR GO; GO:0008464; P:protein modification; IEA.
DR InterPro; IPR004344; Tub_tyr_ligase.
DR Pfam; PF03133; TTL; 1.
KW Hypothetical protein.
SQ SEQUENCE 434 AA; 49433 MW; 9E79E6CA08651CA1 CRC64;

Query Match 2.4%; Score 13; DB 2; Length 434;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 ROWFLVTDWNPFLT 210
Db 126 ROWFLVTDWNPFLT 138

RESULT 12
QARY08 TETNG PRELIMINARY; PRT; 534 AA.
ID QARY08_TETNG
AC QARY08;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 11 SCAF14979, whole genome shotgun sequence.
GN ORFNames=GSTENG00027209001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
[1]
RN NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dessat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
[2]
RN NUCLEOTIDE SEQUENCE.
RP Genoscope; Whitehead Institute Centre for Genome Research;
RG Genoscope; Whitehead Institute Centre for Genome Research.
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAEE01014979; CAG06724.1; -; Genomic DNA.
SQ SEQUENCE 534 AA; 60130 MW; 62B5BBB6965662B CRC64;

Query Match 2.4%; Score 13; DB 2; Length 534;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 ROWFLVTDWNPFLT 210
Db 326 ROWFLVTDWNPFLT 338

```

```

RESULT 13
ID QBV51_MOUSE PRELIMINARY; PRT; 704 AA.
AC QBV51;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
DE library, clone:A630053H17 product:HTL PROTEIN homolog.
GN Name=483344J24Rik;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA The PANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Inotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Nunazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK080321; BAC37878.1; -; mRNA.
DR Ensembl; ENSMUSG00000030276; Mus musculus.
DR MGI; MGI:2141418; 483344J24Rik.
DR GO; GO:0004835; P:tubulin-tyrosine ligase activity; IEA.
DR GO; GO:0006464; P:protein modification; IEA.
DR InterPro; IPR004344; Tub_tyr_ligase.
DR Pfam; PF03133; TTL; 1.
DR SEQUENCE 704 AA; 79080 MW; 3FAD8899C1DB5CF7D CRC64;
Query Match 2.4%; Score 13; DB 2; Length 704;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 198 ROWFLVTDWNPILT 210
DB 308 ROWFLVTDWNPILT 320
|||||
|||||
RESULT 14
QH876_HUMAN
ID QH876_HUMAN PRELIMINARY; PRT; 744 AA.
AC QH876;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ13898.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thyroid gland;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoa K., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiyama S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

```

```
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
DR EMBL; AK023960; BAB1741.1.1; -; mRNA.
DR Ensembl; ENSG00000156983; Homo sapiens.
DR GO; GO:0016874; F:ligase activity; IEA.
DR DR GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA.
DR DR GO; GO:0006464; P:protein modification; IEA.
DR InterPro; IPR004344; Tub_tyr_lygase.
DR Pfam; PF03133; TTL; 1.
KW Ligase.
FT NON_TER 744 744
SQ SEQUENCE 744 AA; 84683 MW; DF661753E4AFF0DF CRC64;

Query Match 2.4%; Score 13; DB 2; Length 744;
Best Local Similarity 100.0%; Pred. No. 0.00079;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 ROWFLVTDNNPLT 210
DB 338 ROWFLVTDNNPLT 350

RESULT 15
Q7Q156 ANOQA
ID Q7Q156 ANOQA PRELIMINARY; PRT; 572 AA.
AC Q7Q156;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP00000022337 (Fragment).
GN CRPNames-ENSANGG00000019848;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008980; EAA13905.2; -; Genomic DNA.
DR GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA.
DR GO; GO:0006464; P:protein modification; IEA.
DR InterPro; IPR004344; Tub_tyr_lygase.
DR Pfam; PF03133; TTL; 1.
FT NON_TER 572 572
FT NON_TER 572 572
SQ SEQUENCE 572 AA; 67109 MW; 8938D9EDD5935071 CRC64;

Query Match 2.2%; Score 12; DB 2; Length 572;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 IWFKESYLRFSS 222
DB 381 IWFKESYLRFSS 392

Search completed: May 15, 2006, 10:01:02
Job time : 94 secs
```



GenCore version 5.1.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2006, 09:57:43 ; Search time 17 Seconds  
(without alignments)  
3061.957 Million cell updates/sec

Title: US-10-635-977-2  
Perfect score: 541  
Sequence: 1 MASSILKVVVSHQSCSRSSR.....LRCLKTAEGALRPPPGKGS 541

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR\_80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	13	2.4	352	T12515	hypothetical prote
2	9	1.7	547	AI0990	methyl-accepting c
3	9	1.7	547	A47178	methyl-accepting t
4	8	1.5	110	D82628	hypothetical prote
5	8	1.5	165	B56535	DNA-damage-inducib
6	8	1.5	264	JC5640	2-hydroxypent-2,4-
7	8	1.5	269	E95999	probable methyl-tr
8	8	1.5	325	G87447	conserved hypotet
9	8	1.5	453	S67089	hypothetical prote
10	8	1.5	503	S21805	portal protein - p
11	8	1.5	513	A87324	hypothetical prote
12	8	1.5	533	T26860	hypothetical prote
13	8	1.5	557	T41495	hypothetical prote
14	8	1.5	830	F83288	conserved hypotet
15	7	1.3	74	I57554	interleukin-3 rece
16	7	1.3	92	S52777	hypothetical prote
17	7	1.3	113	A75626	salicylate monooxy
18	7	1.3	124	S20545	phosphate acceptor
19	7	1.3	130	H8RT2A	histone H2A - rat
20	7	1.3	142	JU0510	fusaric acid resis
21	7	1.3	144	F97044	hypothetical prote
22	7	1.3	162	Z3BP17	gene 3 protein - p
23	7	1.3	162	Z3BP22	gene 3 protein - p
24	7	1.3	169	F75253	conserved hypotet
25	7	1.3	173	T06250	probable resistanc
26	7	1.3	173	AG0587	tail core protein
27	7	1.3	188	C87487	ribosome recycling
28	7	1.3	199	I49745	HMG box protein -
29	7	1.3	205	B95285	conserved hypotet

30	7	1.3	223	2	F98239	hypothetical prote
31	7	1.3	227	2	T07755	disease resistance
32	7	1.3	229	2	F75121	ribose 5-phosphate
33	7	1.3	239	2	AG2643	flagellar L-ring p
34	7	1.3	239	2	G97425	flagellar L-ring p
35	7	1.3	243	2	F69725	tRNA methyltransfe
36	7	1.3	246	2	G83959	methionine aminope
37	7	1.3	251	2	A70113	hypothetical prote
38	7	1.3	253	2	E75493	indole-3-glycerol
39	7	1.3	258	2	E81395	glycine hydroxymet
40	7	1.3	260	2	I40886	hypothetical prote
41	7	1.3	262	2	T05654	ferrichrome transp
42	7	1.3	265	1	QRECFH	hypothetical prote
43	7	1.3	265	2	C90648	hypothetical prote
44	7	1.3	265	2	C85499	hypothetical prote
45	7	1.3	270	2	H83619	hypothetical prote

ALIGNMENTS

RESULT 1

T12515  
hypothetical protein DKFp434B103.1 - human  
C:Species: Homo sapiens (man)  
C>Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 09-Jul-2004  
C:Accession: T12515  
R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, June 1999  
A:Reference number: Z17524  
A:Accession: T12515  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-352 <WMA>  
A:Cross-references: UNIPROT:Q9Y4P7; UNIPARC:UPI00001377A6; EMBL:AL096725  
A:Experimental source: adult testis; clone DKFp434B103  
C:Genetics:  
A>Note: DKFp434B103.1

Query Match 2.4%; Score 13; DB 2; Length 352;  
Best Local Similarity 100.0%; Pred. No. 0.00011;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 RQWFLVTDWNPILT 210

Db 126 RQWFLVTDWNPILT 138

RESULT 2

AI0990  
methyl-accepting chemotaxis citrate transducer [imported] - Salmonella enterica subsp.  
C:Species: Salmonella enterica subsp. enterica serovar Typhi  
A>Note: this species has also been called Salmonella typhi  
C>Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C:Accession: AI0990  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar  
S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.  
A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero  
A:Reference number: AB0502; MUID:21534947; PMID:11677608  
A:Accession: AI0990  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-547 <PAR>  
A:Cross-references: UNIPARC:UPI000005A77D; GB:AL513382; PIDN:CAD08053.1; PID:gl6505033;

A:Gene: STY4234  
C:Superfamily: methyl-accepting chemotaxis protein

Query Match 1.7%; Score 9; DB 2; Length 547;  
Best Local Similarity 100.0%; Pred. No. 1.8;

```

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 AGSSDLSSR 38
   |||||
Db 285 AGSSDLSSR 293

RESULT 3
A47178
methyl-accepting transmembrane citrate/phenol chemoreceptor Tcp - Salmonella typhimurium
C;Species: Salmonella typhimurium
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A47178
R;Yamamoto, K.; Imae, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 217-221, 1993
A;Title: Cloning and characterization of the Salmonella typhimurium-specific chemoreceptor
A;Reference number: A47178; MUID:93126346; PMID:8419927
A;Accession: A47178
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-547 <YAM>
A;Cross-references: UNIPROT:Q02755; UNIPARC:UPI000012BDAA; GB:L06029; NID:g154380; PIDN:
A;Experimental source: ST1
A;Note: sequence extracted from NCBI backbone (NCBIN:122070, NCBI:P122071)
C;Superfamily: methyl-accepting chemotaxis protein
C;Keywords: transmembrane protein

Query Match 1.7%; Score 9; DB 2; Length 547;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 AGSSDLSSR 38
   |||||
Db 285 AGSSDLSSR 293

RESULT 4
D82628
hypothetical protein XF1860 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: D82628
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: D82628
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-110 <SIM>
A;Cross-references: UNIPROT:Q9PCC1; UNIPARC:UPI00000C2866; GB:AE004007; GB:AE003849; NID
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorriy, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigh
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.P.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
A;Genetics:
A;Gene: XF1860

Query Match 1.5%; Score 8; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 438 ALQDLGL 445
   |||||
Db 76 ALQDLGL 83

```

## RESULT 5

B56535

DNA-damage-inducible protein gadd45 - mouse

N;Alternate names: MyD118 protein homolog

C;Species: Mus musculus (house mouse)

C;Date: 19-Oct-1995 #sequence\_revision 19-Oct-1995 #text\_change 09-Jul-2004

C;Accession: B56535; I49679

R;Zhan, Q.; Lord, K.A.; Alamo Jr., I.; Hollander, M.C.; Carrier, F.; Ron, D.; Kohn, K.W.

Mol. Cell. Biol. 14, 2361-2371, 1994

A;Title: The gadd and MyD genes define a novel set of mammalian genes encoding acidic p

A;Reference number: A56535; MUID:94187707; PMID:8139541

A;Accession: B56535

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-165 &lt;ZHA&gt;

A;Cross-references: UNIPROT:P48316; UNIPARC:UPI0000001902; GB:L28177; NID:g456100; PIDN:

R;Alimhanov, M.B.; Kuprash, D.V.; Turetskaya, R.L.; Osipovich, O.A.; Borodulina, O.R.;

Dokl. Akad. Nauk 333, 788-791, 1993

A;Title: Cloning and characteristics of murine genes coding for the human GADD45 analog

A;Reference number: I49679; MUID:94154610; PMID:7509226

A;Accession: I49679

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-165 &lt;RES&gt;

A;Cross-references: UNIPARC:UPI0000001902; EMBL:U00937; NID:g392933; PIDN:AAC27351.1; P

C;Genetics:

A;Gene: Gadd45

A;Introns: 15/2; 49/2; 128/3

C;Superfamily: human DNA-damage-inducible protein gadd45

Query Match 1.5%; Score 8; DB 2; Length 165;

Best Local Similarity 100.0%; Pred. No. 6.9;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 AESGGAAQ 470

|||||

Db 111 AESGGAAQ 118

## RESULT 6

JC5640

2-hydroxy-pent-2,4-dienoate hydratase (EC 4.2.1.-) - Pseudomonas sp.

C;Species: Pseudomonas sp.

C;Date: 27-Oct-1997 #sequence\_revision 27-Oct-1997 #text\_change 09-Jul-2004

C;Accession: JC5640

R;Kim, S.; Kwon, O.K.; Kim, Y.; Kim, C.K.; Lee, K.S.; Kim, Y.C.

Biochem. Biophys. Res. Commun. 238, 56-60, 1997

A;Title: Localization and sequence analysis of the phnH gene encoding 2-hydroxy-pent-2,4-

A;Reference number: JC5640; MUID:97445124; PMID:9299451

A;Accession: JC5640

A;Molecule type: DNA

A;Residues: 1-264 &lt;KIM&gt;

A;Cross-references: UNIPROT:O34721; UNIPARC:UPI00000BA64D; GB:U97697; NID:g2316025; PID

A;Experimental source: strain DJ77

C;Comment: This enzyme is responsible for the conversion of 2-hydroxy-pent-2,4-dienoate

C;Genetics:

A;Gene: phnH

C;Superfamily: 2-hydroxy-penta-2,4-dienoate hydratase

C;Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 1.5%; Score 8; DB 2; Length 264;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 459 LRGAESG 466

|||||

Db 15 LRGAESG 22

RESULT 7  
E95999  
probable methyl-transferase, S-Adenosyl-L-methionine (SAM)-MTase protein [imported] - *Sinorhizobium meliloti*  
C:Species: *Sinorhizobium meliloti*  
C>Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 12-Jul-2004  
C:Accession: E95999  
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan  
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo  
A:Reference number: A95842; MUID:21396508; PMID:11481431  
A:Accession: E95999  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-269 <KUP>  
A:Cross-references: UNIPROT:Q92U77; UNIPARC:UPI00000D4790; GB:AL591985; PIDN:CAC49661.1;  
A:Experimental source: strain 1021, megaplasmid pSymB  
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kies, E.; Komp, C.; Lelaure,  
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.  
A:Reference number: A96039; MUID:21368234; PMID:11474104  
A:Contents: annotation  
C:Genetics:  
A:Gene: SMB21433  
A:Genome: plasmid  
C:Superfamily: spore germination protein C2

Query Match 1.5%; Score 8; DB 2; Length 269;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 146 AKSRGRDI 153  
Db 98 AKSRGRDI 105  
RESULT 8  
G87447  
conserved hypothetical protein CC1600 [imported] - *Caulobacter crescentus*  
C:Species: *Caulobacter crescentus*  
C>Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C:Accession: G87447  
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of *Caulobacter crescentus*.  
A:Reference number: A87249; MUID:21173698; PMID:11259647  
A:Accession: G87447  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-325 <STO>  
A:Cross-references: UNIPROT:Q9A7W9; UNIPARC:UPI00000C7438; GB:AE005673; NID:G13422997; E  
C:Genetics:  
A:Gene: CC1600

Query Match 1.5%; Score 8; DB 2; Length 325;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 391 GVSRRAR 398  
Db 279 GVSRRAR 286

RESULT 9  
S67089  
hypothetical protein YOR197w - yeast (*Saccharomyces cerevisiae*)

N:Alternate names: hypothetical protein O4814  
C:Species: *Saccharomyces cerevisiae*  
C>Date: 12-Jul-1996 #sequence\_revision 12-Jul-1996 #text\_change 31-Dec-2004  
C:Accession: S67089  
R:Hughes, B.; Pohl, T.M.  
submitted to the Protein Sequence Database, July 1996  
A:Reference number: S66685  
A:Accession: S67089  
A:Molecule type: DNA  
A:Residues: 1-453 <HUG>  
A:Cross-references: UNIPROT:Q08601; UNIPARC:UPI00000698BA; EMBL:Z75105; NID:G1420468; P  
A:Experimental source: strain S288C  
C:Genetics:  
A:Gene: MIPS:YOR197w  
A:Cross-references: SGD:S0005723  
A:Map position: 15R  
C:Superfamily: Metacaspase

Query Match 1.5%; Score 8; DB 2; Length 453;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 77 TSADAVED 84  
Db 388 TSADAVED 395

RESULT 10  
S21805  
portal protein - phage SPPI  
N:Alternate names: gene 6 protein  
C:Species: phage SPPI  
C>Date: 22-Nov-1993 #sequence\_revision 12-Apr-1996 #text\_change 09-Jul-2004  
C:Accession: S21805; S24455; T42270; S36725  
R:Tavares, P.; Santos, M.A.; Lurz, R.; Morelli, G.; de Lencastre, H.; Trautner, T.A.  
J. Mol. Biol. 225, 81-92, 1992  
A:Title: Identification of a gene in *Bacillus subtilis* bacteriophage SPPI determining ti  
A:Reference number: S21805; MUID:92260540; PMID:1583695  
A:Accession: S21805  
A:Molecule type: DNA  
A:Residues: 1-503 <TAV>  
A:Cross-references: UNIPROT:P54309; UNIPARC:UPI00001359D0; EMBL:X56064; NID:G15464; PID  
R:Chai, S.; Bravo, A.; Lueder, G.; Nedlin, A.; Trautner, T.A.; Alonso, J.C.  
J. Mol. Biol. 224, 87-102, 1992  
A:Title: Molecular analysis of the *Bacillus subtilis* bacteriophage SPPI region encompass  
A:Reference number: S24450; MUID:92194332; PMID:1548711  
A:Accession: S24455  
A:Molecule type: DNA  
A:Residues: 1-37 <CHA>  
A:Cross-references: UNIPARC:UPI000017A851; EMBL:X56064  
R:Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A.  
Gene 204, 201-212, 1997  
A:Title: The complete nucleotide sequence and functional organization of *Bacillus subtili*  
A:Reference number: S22137; MUID:98094274; PMID:9434185  
A:Accession: T42270  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-503 <ALO>  
A:Cross-references: UNIPARC:UPI00001359D0; EMBL:X97918; PIDN:CAA66580.1  
C:Genetics:  
A:Gene: 6

Query Match 1.5%; Score 8; DB 2; Length 503;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 461 GAAESGGA 468  
Db 492 GAAESGGA 499

RESULT 11  
A87324

```
hypothetical protein CC0603 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: A87324
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Winn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87324
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-513 <STO>
A;Cross-references: UNIPROT:Q9AAJ4; UNIPARC:UPI00000C70DC; GB:AE005673; NID:G13421807; F
C;Genetics:
A;Gene: CC0603

Query Match 1.5%; Score 8; DB 2; Length 513;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 406 NLKASL 413
Db 308 NLKASL 315
|||||

RESULT 12
T26860
hypothetical protein Y43F8B.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26860
R;Ainscough, R.
submitted to the EMBL Data Library, October 1998
A;Reference number: Z20278
A;Accession: T26860
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-533 <WIL>
A;Cross-references: UNIPROT:Q9WX4; UNIPARC:UPI000007A7D5; EMBL:AL032623; PIDN:CAA21512.
A;Experimental source: clone Y43F8B
C;Genetics:
A;Gene: CESP:Y43F8B.4
A;Introns: 48/1; 100/3; 201/1; 257/2; 350/3; 483/3

Query Match 1.5%; Score 8; DB 2; Length 533;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 GAIESGGA 468
Db 447 GAIESGGA 454
|||||

RESULT 13
T41495
hypothetical protein SPC622.15c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T41495
R;Seeger, K.; Harris, D.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1998
A;Reference number: Z21998
A;Accession: T41495
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-557 <SEE>
A;Cross-references: UNIPROT:Q94602; UNIPARC:UPI000006A248; EMBL:AL033127; PIDN:CAA21871.
A;Experimental source: strain 972h-; cosmid c622
C;Genetics:
A;Gene: SPDB:SPC622.15c
A;Map position: 3
```

```
Query Match 1.5%; Score 8; DB 2; Length 557;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 PPPFSGSD 386
Db 483 PPPFSGSD 490
|||||

RESULT 14
F83288
conserved hypothetical protein PA2858 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: F83288
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F83288
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-830 <STO>
A;Cross-references: UNIPROT:Q9HZY6; UNIPARC:UPI00000C5849; GB:AE004712; GB:AE004091; NI
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA2858
C;Superfamily: Escherichia coli probable membrane protein ybbP

Query Match 1.5%; Score 8; DB 2; Length 830;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 438 ALQDLGL 445
Db 563 ALQDLGL 570
|||||

RESULT 15
I57554
interleukin-3 receptor beta subunit - mouse (fragment)
C;Species: Mus sp. (mouse)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I57554
R;Hannemann, J.; Hara, T.; Kawai, M.; Miyajima, A.; Ostertag, W.; Stocking, C.
Mol. Cell. Biol. 15, 2402-2412, 1995
A;Title: Sequential mutations in the interleukin-3 (IL3)/granulocyte-macrophage colony-
mediated by a truncated beta C subunit.
A;Reference number: I57554; MUID:95257920; PMID:7739524
A;Accession: I57554
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-74 <RES>
A;Cross-references: UNIPROT:Q64130; UNIPARC:UPI00000E599C; GB:S78451; NID:G998544; PIDN:
C;Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor;

Query Match 1.3%; Score 7; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 420 KARGPSA 426
Db 16 KARGPSA 22
|||||

Search completed: May 15, 2006, 09:58:09
Job time : 19 secs
```

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

# OM protein - protein search, using sw model

Run on: May 15, 2006, 09:58:33 ; Search time 52 Seconds  
(without alignments)  
488.448 Million cell updates/sec

Title: US-10-635-977-2

Perfect score: 541

Sequence: 1 MASSILKVVSHQSCRSRR.....LRGLKTARGLRPPPGKGS 541

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 250354 seqs, 46948837 residues

Word size : 1

Total number of hits satisfying chosen parameters: 250120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications\_AA\_New:\*

- 1: /SIDSS/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.1\*
- 2: /SIDSS/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.2\*
- 3: /SIDSS/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.3\*
- 4: /SIDSS/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.4\*
- 5: /SIDSS/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.5\*
- 6: /SIDSS/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.6\*
- 7: /SIDSS/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.7\*
- 8: /SIDSS/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.8\*
- 9: /SIDSS/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.9\*
- 10: /SIDSS/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.10\*
- 11: /SIDSS/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.11\*
- 12: /SIDSS/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.12\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	1.5	113	9	US-10-784-004-1238
2	8	1.5	165	10	US-11-297-160-8
3	8	1.5	181	11	US-11-175-690-344
4	8	1.5	181	11	US-11-175-690-345
5	8	1.5	181	11	US-11-175-690-346
6	8	1.5	181	11	US-11-175-690-347
7	8	1.5	181	11	US-11-175-690-348
8	8	1.5	181	11	US-11-175-690-349
9	8	1.5	261	11	US-11-096-568A-20320
10	8	1.5	790	11	US-11-175-690-257
11	8	1.5	790	11	US-11-175-690-258
12	8	1.5	790	11	US-11-175-690-259
13	8	1.5	790	11	US-11-175-690-260
14	8	1.5	790	11	US-11-175-690-261
15	8	1.5	790	11	US-11-175-690-262
16	8	1.5	985	9	US-10-532-482-60
17	8	1.5	997	9	US-10-532-482-58
18	8	1.5	1004	9	US-10-532-482-59
19	8	1.5	1013	9	US-10-532-482-32
20	8	1.5	1016	9	US-10-532-482-57
21	8	1.5	1032	9	US-10-532-482-56

Sequence 884, App  
Sequence 11159, A  
Sequence 16, Appl  
Sequence 30, Appl  
Sequence 2, Appl  
Sequence 1006, Ap  
Sequence 9822, Ap  
Sequence 23722, Ap  
Sequence 17748, A  
Sequence 9010, Ap  
Sequence 23721, A  
Sequence 25745, A  
Sequence 21131, A  
Sequence 7616, Ap  
Sequence 7479, Ap  
Sequence 23720, A  
Sequence 25744, A  
Sequence 16519, A  
Sequence 1006, Ap  
Sequence 20771, A  
Sequence 4398, Ap  
Sequence 7464, Ap  
Sequence 3606, Ap  
Sequence 2545, Ap

## ALIGNMENTS

### RESULT 1

US-10-784-004-1238  
; Sequence 1238, Application US/10784004  
; Publication No. US20060084066A1  
; GENERAL INFORMATION:  
; APPLICANT: Biogen Idec  
; TITLE OF INVENTION: Surrogate Markers of Pain  
; FILE REFERENCE: 08201.6029-00000  
; CURRENT APPLICATION NUMBER: US/10/784,004  
; CURRENT FILING DATE: 2004-02-20  
; NUMBER OF SEQ ID NOS: 1251  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1238  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: human  
US-10-784-004-1238

Query Match 1.5%; Score 8; DB 9; Length 113;  
Best Local Similarity 100.0%; Pred. No. 2.6;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 530 GALRPPPG 537  
Db 65 GALRPPPG 72

### RESULT 2

US-11-297-160-8  
; Sequence 8, Application US/11297160  
; Publication No. US2006008888A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Xin Wei  
; APPLICANT: Harris, Curtis C.  
; APPLICANT: Fornace Jr., Albert J.  
; APPLICANT: Zhan, Qimin  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by the Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Methods for Identifying Inhibitors of GADD45  
; FILE REFERENCE: 015280-367100US  
; CURRENT APPLICATION NUMBER: US/11/297,160

```
; CURRENT FILING DATE: 2005-12-07
; PRIOR APPLICATION NUMBER: US/10/600,158
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US/09/534,811
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,069
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: mouse growth arrest and DNA-damage-inducible
; OTHER INFORMATION: protein (mgADD45)
US-11-297-160-8

Query Match 1.5%; Score 8; DB 10; Length 165;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 AESGGAQ 470
      |||||
Db 111 AESGGAQ 118

RESULT 3
US-11-175-690-344
; Sequence 344, Application US/11/175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 344
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-344

Query Match 1.5%; Score 8; DB 11; Length 181;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 530 GALRPPPG 537
      |||||
Db 133 GALRPPPG 140

RESULT 5
US-11-175-690-346
; Sequence 346, Application US/11/175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 346
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-346

Query Match 1.5%; Score 8; DB 11; Length 181;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 530 GALRPPPG 537
      |||||
Db 133 GALRPPPG 140

RESULT 4
US-11-175-690-345
; Sequence 345, Application US/11/175690
```

Query Match 1.5%; Score 8; DB 11; Length 181;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 8; Conservative 0; Mismatches 0; Gaps 0;  
Indels 0;

QY 530 GALTREPPG 537  
DB 133 GALTREPPG 140

## RESULT 6

US-11-175-690-347  
Sequence 347, Application US/11175690  
Publication No. US20060014254A1

GENERAL INFORMATION:  
APPLICANT: Haseltine et al.

TITLE OF INVENTION: Albumin Fusion Proteins

FILE REFERENCE: PF605

CURRENT APPLICATION NUMBER: US/11/175,690

PRIOR FILING DATE: 2005-07-07

PRIOR APPLICATION NUMBER: PCT/US04/001369

PRIOR FILING DATE: 2004-01-20

PRIOR APPLICATION NUMBER: US 60/441,305

PRIOR FILING DATE: 2003-01-22

PRIOR APPLICATION NUMBER: US 60/453,201

PRIOR FILING DATE: 2003-03-11

PRIOR APPLICATION NUMBER: US 60/467,222

PRIOR FILING DATE: 2003-05-02

PRIOR APPLICATION NUMBER: US 60/472,816

PRIOR FILING DATE: 2003-05-23

PRIOR APPLICATION NUMBER: US 60/476,267

PRIOR FILING DATE: 2003-06-06

PRIOR APPLICATION NUMBER: US 60/505,172

PRIOR FILING DATE: 2003-09-24

PRIOR APPLICATION NUMBER: US 60/506,746

PRIOR FILING DATE: 2003-09-30

NUMBER OF SEQ ID NOS: 568

SOFTWARE: Patent in Ver. 2.0

SEQ ID NO 347

LENGTH: 181

TYPE: PRT

ORGANISM: Homo sapiens

US-11-175-690-347

Query Match 1.5%; Score 8; DB 11; Length 181;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 8; Conservative 0; Mismatches 0; Gaps 0;  
Indels 0;

QY 530 GALTREPPG 537  
DB 133 GALTREPPG 140

## RESULT 7

US-11-175-690-348

Sequence 348, Application US/11175690

Publication No. US20060014254A1

GENERAL INFORMATION:  
APPLICANT: Haseltine et al.

TITLE OF INVENTION: Albumin Fusion Proteins

FILE REFERENCE: PF605

CURRENT APPLICATION NUMBER: US/11/175,690

PRIOR FILING DATE: 2005-07-07

PRIOR APPLICATION NUMBER: PCT/US04/001369

PRIOR FILING DATE: 2004-01-20

PRIOR APPLICATION NUMBER: US 60/441,305

PRIOR FILING DATE: 2003-01-22

PRIOR APPLICATION NUMBER: US 60/453,201

PRIOR FILING DATE: 2003-03-11

PRIOR APPLICATION NUMBER: US 60/467,222

PRIOR FILING DATE: 2003-05-02

PRIOR APPLICATION NUMBER: US 60/472,816

PRIOR FILING DATE: 2003-05-23

PRIOR APPLICATION NUMBER: US 60/476,267  
PRIOR FILING DATE: 2003-06-06  
PRIOR APPLICATION NUMBER: US 60/505,172  
PRIOR FILING DATE: 2003-09-24  
PRIOR APPLICATION NUMBER: US 60/506,746  
PRIOR FILING DATE: 2003-09-30  
NUMBER OF SEQ ID NOS: 568  
SOFTWARE: Patent in Ver. 2.0  
SEQ ID NO 348  
LENGTH: 181  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-175-690-348

Query Match 1.5%; Score 8; DB 11; Length 181;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 8; Conservative 0; Mismatches 0; Gaps 0;  
Indels 0;

QY 530 GALTREPPG 537  
DB 133 GALTREPPG 140

## RESULT 8

US-11-175-690-349

Sequence 349, Application US/11175690

Publication No. US20060014254A1

GENERAL INFORMATION:  
APPLICANT: Haseltine et al.

TITLE OF INVENTION: Albumin Fusion Proteins

FILE REFERENCE: PF605

CURRENT APPLICATION NUMBER: US/11/175,690

PRIOR FILING DATE: 2005-07-07

PRIOR APPLICATION NUMBER: PCT/US04/001369

PRIOR FILING DATE: 2004-01-20

PRIOR APPLICATION NUMBER: US 60/441,305

PRIOR FILING DATE: 2003-01-22

PRIOR APPLICATION NUMBER: US 60/453,201

PRIOR FILING DATE: 2003-03-11

PRIOR APPLICATION NUMBER: US 60/467,222

PRIOR FILING DATE: 2003-05-02

PRIOR APPLICATION NUMBER: US 60/472,816

PRIOR FILING DATE: 2003-05-23

PRIOR APPLICATION NUMBER: US 60/476,267

PRIOR FILING DATE: 2003-06-06

PRIOR APPLICATION NUMBER: US 60/505,172

PRIOR FILING DATE: 2003-09-24

PRIOR APPLICATION NUMBER: US 60/506,746

PRIOR FILING DATE: 2003-09-30

NUMBER OF SEQ ID NOS: 568

SOFTWARE: Patent in Ver. 2.0

SEQ ID NO 349

LENGTH: 181

TYPE: PRT

ORGANISM: Homo sapiens

US-11-175-690-349

Query Match 1.5%; Score 8; DB 11; Length 181;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 8; Conservative 0; Mismatches 0; Gaps 0;  
Indels 0;

QY 530 GALTREPPG 537  
DB 133 GALTREPPG 140

## RESULT 9

US-11-096-568A-20320

Sequence 20320, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:  
APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

```
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20320
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(261)
; OTHER INFORMATION: Ceres Seq. ID no. 12381376
US-11-096-568A-20320
```

```
Query Match 1.5%; Score 8; DB 11; Length 261;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 431 AOGPPSPA 438
| | | | |
Db 161 AOGPPSPA 168
```

## RESULT 10

```
US-11-175-690-257
; Sequence 257, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 257
; LENGTH: 790
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-257
```

```
Query Match 1.5%; Score 8; DB 11; Length 790;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 530 GALRPPPG 537
| | | | |
Db 742 GALRPPPG 749
```

## RESULT 11

```
US-11-175-690-258
; Sequence 258, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
```

```
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 258
; LENGTH: 790
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-258
```

```
Query Match 1.5%; Score 8; DB 11; Length 790;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 530 GALRPPPG 537
| | | | |
Db 157 GALRPPPG 164
```

## RESULT 12

```
US-11-175-690-259
; Sequence 259, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 259
; LENGTH: 790
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-259
```

```
Query Match 1.5%; Score 8; DB 11; Length 790;
Best Local Similarity 100.0%; Pred. No. 17;
```



Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 530 GALTTPPG 537  
|||||  
Db 742 GALTTPPG 749

## RESULT 13

US-11-175-690-260  
; Sequence 260, Application US/11175690  
; Publication No. US20060014254A1  
; GENERAL INFORMATION:  
; APPLICANT: Haseltine et al.  
; TITLE OF INVENTION: Albumin Fusion Proteins  
; FILE REFERENCE: PF605  
; CURRENT APPLICATION NUMBER: US/11/175,690  
; PRIOR FILING DATE: 2005-07-07  
; PRIOR APPLICATION NUMBER: PCT/US04/001369  
; PRIOR FILING DATE: 2004-01-20  
; PRIOR APPLICATION NUMBER: US 60/441,305  
; PRIOR FILING DATE: 2003-01-22  
; PRIOR APPLICATION NUMBER: US 60/453,201  
; PRIOR FILING DATE: 2003-03-11  
; PRIOR APPLICATION NUMBER: US 60/467,222  
; PRIOR FILING DATE: 2003-05-02  
; PRIOR APPLICATION NUMBER: US 60/472,816  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: US 60/476,267  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: US 60/505,172  
; PRIOR FILING DATE: 2003-09-24  
; PRIOR APPLICATION NUMBER: US 60/506,746  
; PRIOR FILING DATE: 2003-09-30  
; NUMBER OF SEQ ID NOS: 568  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 260  
; LENGTH: 790  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-175-690-260

Query Match 1.5%; Score 8; DB 11; Length 790;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 530 GALTTPPG 537  
|||||  
Db 157 GALTTPPG 164

## RESULT 14

US-11-175-690-261  
; Sequence 261, Application US/11175690  
; Publication No. US20060014254A1  
; GENERAL INFORMATION:  
; APPLICANT: Haseltine et al.  
; TITLE OF INVENTION: Albumin Fusion Proteins  
; FILE REFERENCE: PF605  
; CURRENT APPLICATION NUMBER: US/11/175,690  
; PRIOR FILING DATE: 2005-07-07  
; PRIOR APPLICATION NUMBER: PCT/US04/001369  
; PRIOR FILING DATE: 2004-01-20  
; PRIOR APPLICATION NUMBER: US 60/441,305  
; PRIOR FILING DATE: 2003-01-22  
; PRIOR APPLICATION NUMBER: US 60/453,201  
; PRIOR FILING DATE: 2003-03-11  
; PRIOR APPLICATION NUMBER: US 60/467,222  
; PRIOR FILING DATE: 2003-05-02  
; PRIOR APPLICATION NUMBER: US 60/472,816  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: US 60/476,267  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: US 60/505,172

; PRIOR FILING DATE: 2003-09-24  
; PRIOR APPLICATION NUMBER: US 60/506,746  
; PRIOR FILING DATE: 2003-09-30  
; NUMBER OF SEQ ID NOS: 568  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 261  
; LENGTH: 790  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-175-690-261

Query Match 1.5%; Score 8; DB 11; Length 790;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 530 GALTTPPG 537  
|||||  
Db 742 GALTTPPG 749

## RESULT 15

US-11-175-690-262  
; Sequence 262, Application US/11175690  
; Publication No. US20060014254A1  
; GENERAL INFORMATION:  
; APPLICANT: Haseltine et al.  
; FILE REFERENCE: PF605  
; CURRENT APPLICATION NUMBER: US/11/175,690  
; PRIOR FILING DATE: 2005-07-07  
; PRIOR APPLICATION NUMBER: PCT/US04/001369  
; PRIOR FILING DATE: 2004-01-20  
; PRIOR APPLICATION NUMBER: US 60/441,305  
; PRIOR FILING DATE: 2003-01-22  
; PRIOR APPLICATION NUMBER: US 60/453,201  
; PRIOR FILING DATE: 2003-03-11  
; PRIOR APPLICATION NUMBER: US 60/467,222  
; PRIOR FILING DATE: 2003-05-02  
; PRIOR APPLICATION NUMBER: US 60/472,816  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: US 60/476,267  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: US 60/505,172  
; PRIOR FILING DATE: 2003-09-24  
; PRIOR APPLICATION NUMBER: US 60/506,746  
; NUMBER OF SEQ ID NOS: 568  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 262  
; LENGTH: 790  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-175-690-262

Query Match 1.5%; Score 8; DB 11; Length 790;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 530 GALTTPPG 537  
|||||  
Db 157 GALTTPPG 164

Search completed: May 15, 2006, 09:59:33  
Job time : 53 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2006, 09:58:23 ; Search time 85 Seconds  
(without alignments)  
2659.361 Million cell updates/sec

Title: US-10-635-977-2  
Perfect score: 541  
Sequence: 1 MASSILKVVSHQSCSRSSR.....LRGLKTARCALRPPPGKRGKS 541

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 1

Total number of hits satisfying chosen parameters: 1866650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA Main:  
1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/prodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

*length*  
*Query*  
*Match*

Result No.	Score	Query Match	Length	ID	Description
1	541	100.0	541	US-10-615-659-2	Sequence 2, Appli
2	541	100.0	541	US-10-635-977-2	Sequence 2, Appli
3	514	95.0	541	US-10-615-659-13	Sequence 13, Appl
4	514	95.0	541	US-10-635-977-13	Sequence 13, Appl
5	293	54.2	293	US-10-615-659-14	Sequence 14, Appl
6	293	54.2	293	US-10-635-977-14	Sequence 14, Appl
7	242	44.7	242	US-10-615-659-4	Sequence 4, Appli
8	242	44.7	242	US-10-635-977-4	Sequence 4, Appli
9	49	9.1	49	US-10-615-659-21	Sequence 21, Appl
10	49	9.1	49	US-10-615-659-22	Sequence 21, Appl
11	49	9.1	49	US-10-635-977-21	Sequence 21, Appl
12	49	9.1	49	US-10-635-977-22	Sequence 22, Appl
13	42	7.8	42	US-10-615-659-24	Sequence 24, Appl
14	42	7.8	42	US-10-635-977-24	Sequence 24, Appl
15	26	4.8	26	US-10-615-659-23	Sequence 23, Appl
16	26	4.8	26	US-10-635-977-23	Sequence 23, Appl
17	23	4.3	23	US-10-615-659-19	Sequence 19, Appl
18	23	4.3	23	US-10-635-977-19	Sequence 19, Appl
19	17	3.1	17	US-10-615-659-25	Sequence 25, Appl
20	17	3.1	17	US-10-635-977-25	Sequence 25, Appl
21	16	3.0	16	US-10-615-659-46	Sequence 46, Appl
22	16	3.0	16	US-10-615-659-47	Sequence 47, Appl
23	16	3.0	16	US-10-615-659-48	Sequence 48, Appl
24	16	3.0	16	US-10-615-659-49	Sequence 49, Appl
25	16	3.0	16	US-10-615-659-50	Sequence 50, Appl
26	16	3.0	16	US-10-615-659-51	Sequence 51, Appl
27	16	3.0	16	US-10-635-977-46	Sequence 46, Appl

28	16	3.0	16	4	US-10-635-977-47	Sequence 47, Appl
29	16	3.0	16	4	US-10-635-977-48	Sequence 48, Appl
30	16	3.0	16	4	US-10-635-977-49	Sequence 49, Appl
31	16	3.0	16	4	US-10-635-977-50	Sequence 50, Appl
32	16	3.0	16	4	US-10-635-977-51	Sequence 51, Appl
33	14	2.6	14	4	US-10-615-659-38	Sequence 38, Appl
34	14	2.6	14	4	US-10-615-659-39	Sequence 39, Appl
35	14	2.6	14	4	US-10-615-659-40	Sequence 40, Appl
36	14	2.6	14	4	US-10-615-659-41	Sequence 41, Appl
37	14	2.6	14	4	US-10-615-659-42	Sequence 42, Appl
38	14	2.6	14	4	US-10-615-659-43	Sequence 43, Appl
39	14	2.6	14	4	US-10-615-659-44	Sequence 44, Appl
40	14	2.6	14	4	US-10-615-659-45	Sequence 45, Appl
41	14	2.6	14	4	US-10-635-977-38	Sequence 38, Appl
42	14	2.6	14	4	US-10-635-977-39	Sequence 39, Appl
43	14	2.6	14	4	US-10-635-977-40	Sequence 40, Appl
44	14	2.6	14	4	US-10-635-977-41	Sequence 41, Appl
45	14	2.6	14	4	US-10-635-977-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1

US-10-615-659-2  
; Sequence 2, Application US/10615659  
; Publication No. US20040157234A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN  
; FILE REFERENCE: D0283 NP  
; CURRENT APPLICATION NUMBER: US/10/615,659  
; PRIORITY FILING DATE: 2003-07-09  
; PRIOR APPLICATION NUMBER: U.S. 60/394,725  
; PRIOR FILING DATE: 2002-07-09  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 541  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-615-659-2

Query Match	100.0%	Score 541;	DB 4;	Length 541;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 541;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MASSILKVVSHQSCSRSSRKPDRQBEAGSSDLSSRQDAENAEAKRLGQLVADIAC	60	
Db	1	MASSILKVVSHQSCSRSSRKPDRQBEAGSSDLSSRQDAENAEAKRLGQLVADIAC	60	
Qy	61	KVCQAYLQLEHEDTSDA VEDL TEAEWEDLTQOYVSLVHGDAFINSRNYFSOCQAL	120	
Db	61	KVCQAYLQLEHEDTSDA VEDL TEAEWEDLTQOYVSLVHGDAFINSRNYFSOCQAL	120	
Qy	121	LNRIITSVNPQTDIGLRNIWIKPAKSGRGRDIVCMRDRVEEILELAAADHPLSRNKNVY	180	
Db	121	LNRIITSVNPQTDIGLRNIWIKPAKSGRGRDIVCMRDRVEEILELAAADHPLSRNKNVY	180	
Qy	181	QKYIETPLLICDTKFDIRQWFLVTDWNPPLTIWFKYESYLFSTQFSLDKLSAHLNKN	240	
Db	181	QKYIETPLLICDTKFDIRQWFLVTDWNPPLTIWFKYESYLFSTQFSLDKLSAHLNKN	240	
Qy	241	AVQYKLVNDVGRSPLLPAAHNMWTSRFBQYLRQGRGAVGWSVIYPSMKKATAHAMKVAQ	300	
Db	241	AVQYKLVNDVGRSPLLPAAHNMWTSRFBQYLRQGRGAVGWSVIYPSMKKATAHAMKVAQ	300	
Qy	301	DHVEPRKNSFELYGADFLVGRDRFRPWLTEINSSPTMHPSTPTVTAQLCAQVQEDTIKVAVD	360	
Db	301	DHVEPRKNSFELYGADFLVGRDRFRPWLTEINSSPTMHPSTPTVTAQLCAQVQEDTIKVAVD	360	
Qy	361	RSCDIGNFELLWRQPVVEPPFPFSGSDLCVAGSVRRARRQVLPVNCNLKASALLDAQPLK	420	

Db 361 RSCDIGNFELLWQPVVPPFSGSDLCVAGSVRRARRQVLPVCNLKASASLLDAQPLK 420  
QY 421 ARGPSAMPDPAQPPSPALQDRLGLKEEKGPLALLAPLRGAESGAAQPTRTKAAGKV 480  
Db 421 ARGPSAMPDPAQPPSPALQDRLGLKEEKGPLALLAPLRGAESGAAQPTRTKAAGKV 480  
QY 481 ELPACPCRHHVDSQAPNTGVPVAPAKSWDPNQLNAHPLEPVLRLGLTKTAEGALRPPPGGKG 540  
Db 481 ELPACPCRHHVDSQAPNTGVPVAPAKSWDPNQLNAHPLEPVLRLGLTKTAEGALRPPPGGKG 540  
QY 541 S 541  
Db 541 S 541

## RESULT 2

US-10-635-977-2  
; Sequence 2, Application US/10635977  
; Publication No. US20040171131A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN  
; TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42  
; FILE REFERENCE: D0283A CIP  
; CURRENT APPLICATION NUMBER: US/10/635,977  
; PRIOR FILING DATE: 2003-08-07  
; PRIOR APPLICATION NUMBER: U.S. 60/394,725  
; PRIOR FILING DATE: 2002-07-09  
; PRIOR APPLICATION NUMBER: U.S. 10/615,659  
; PRIOR FILING DATE: 2003-07-09  
; NUMBER OF SEQ ID NOS: 103  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 541  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-635-977-2

Query Match 100.0%; Score 541; DB 4; Length 541;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASSILKWVSHQSCSRSSKPRDQREAEAGSSDLSSRQDAENAEAKLRGLPGQLVDIAC 60  
Db 1 MASSILKWVSHQSCSRSSKPRDQREAEAGSSDLSSRQDAENAEAKLRGLPGQLVDIAC 60  
QY 61 KVCQAYLGQLEHEDIDTSADAVEDLTEAEWEDLTQYYSLVHGDAFISNSRNYFSQCOAL 120  
Db 61 KVCQAYLGQLEHEDIDTSADAVEDLTEAEWEDLTQYYSLVHGDAFISNSRNYFSQCOAL 120  
QY 121 LNRITSVNPQTDIDGLRNIWIIPAAKSRGRDIVCMRVEEILELAAADHPLSRDNKVV 180  
Db 121 LNRITSVNPQTDIDGLRNIWIIPAAKSRGRDIVCMRVEEILELAAADHPLSRDNKVV 180  
QY 181 QKYIETPLLCIDTKFDIRQWFLVTDWNPMTIWFYKESYLRFSTQRFSLDKLDSAIHLCNN 240  
Db 181 QKYIETPLLCIDTKFDIRQWFLVTDWNPMTIWFYKESYLRFSTQRFSLDKLDSAIHLCNN 240  
QY 241 AVQKYLKNDVGRSPLLPAHNMMWTSRFOEYLQQRGAVGWSVIYPSMKKAIHAAMKVAQ 300  
Db 241 AVQKYLKNDVGRSPLLPAHNMMWTSRFOEYLQQRGAVGWSVIYPSMKKAIHAAMKVAQ 300  
QY 301 DHVEPRKNSFELYGADFVLGRDFPWLIEINSSPTMHPSTPVTQAQLCAQVQEDTIKVAVD 360  
Db 301 DHVEPRKNSFELYGADFVLGRDFPWLIEINSSPTMHPSTPVTQAQLCAQVQEDTIKVAVD 360  
QY 361 RSCDIGNFELLWQPVVPPFSGSDLCVAGSVRRARRQVLPVCNLKASASLLDAQPLK 420  
Db 361 RSCDIGNFELLWQPVVPPFSGSDLCVAGSVRRARRQVLPVCNLKASASLLDAQPLK 420  
QY 421 ARGPSAMPDPAQPPSPALQDRLGLKEEKGPLALLAPLRGAESGAAQPTRTKAAGKV 480

Db 421 ARGPSAMPDPAQPPSPALQDRLGLKEEKGPLALLAPLRGAESGAAQPTRTKAAGKV 480  
QY 481 ELPACPCRHHVDSQAPNTGVPVAPAKSWDPNQLNAHPLEPVLRLGLTKTAEGALRPPPGGKG 540  
Db 481 ELPACPCRHHVDSQAPNTGVPVAPAKSWDPNQLNAHPLEPVLRLGLTKTAEGALRPPPGGKG 540  
QY 541 S 541  
Db 541 S 541

## RESULT 3

US-10-615-659-13  
; Sequence 13, Application US/10615659  
; Publication No. US20040157234A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN  
; TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42  
; FILE REFERENCE: D0283 NP  
; CURRENT APPLICATION NUMBER: US/10/615,659  
; PRIOR FILING DATE: 2003-07-09  
; PRIOR APPLICATION NUMBER: U.S. 60/394,725  
; PRIOR FILING DATE: 2002-07-09  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 13  
; LENGTH: 541  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-615-659-13

Query Match 95.0%; Score 514; DB 4; Length 541;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASSILKWVSHQSCSRSSKPRDQREAEAGSSDLSSRQDAENAEAKLRGLPGQLVDIAC 60  
Db 1 MASSILKWVSHQSCSRSSKPRDQREAEAGSSDLSSRQDAENAEAKLRGLPGQLVDIAC 60  
QY 61 KVCQAYLGQLEHEDIDTSADAVEDLTEAEWEDLTQYYSLVHGDAFISNSRNYFSQCOAL 120  
Db 61 KVCQAYLGQLEHEDIDTSADAVEDLTEAEWEDLTQYYSLVHGDAFISNSRNYFSQCOAL 120  
QY 121 LNRITSVNPQTDIDGLRNIWIIPAAKSRGRDIVCMRVEEILELAAADHPLSRDNKVV 180  
Db 121 LNRITSVNPQTDIDGLRNIWIIPAAKSRGRDIVCMRVEEILELAAADHPLSRDNKVV 180  
QY 181 QKYIETPLLCIDTKFDIRQWFLVTDWNPMTIWFYKESYLRFSTQRFSLDKLDSAIHLCNN 240  
Db 181 QKYIETPLLCIDTKFDIRQWFLVTDWNPMTIWFYKESYLRFSTQRFSLDKLDSAIHLCNN 240  
QY 241 AVQKYLKNDVGRSPLLPAHNMMWTSRFOEYLQQRGAVGWSVIYPSMKKAIHAAMKVAQ 300  
Db 241 AVQKYLKNDVGRSPLLPAHNMMWTSRFOEYLQQRGAVGWSVIYPSMKKAIHAAMKVAQ 300  
QY 301 DHVEPRKNSFELYGADFVLGRDFPWLIEINSSPTMHPSTPVTQAQLCAQVQEDTIKVAVD 360  
Db 301 DHVEPRKNSFELYGADFVLGRDFPWLIEINSSPTMHPSTPVTQAQLCAQVQEDTIKVAVD 360  
QY 361 RSCDIGNFELLWQPVVPPFSGSDLCVAGSVRRARRQVLPVCNLKASASLLDAQPLK 420  
Db 361 RSCDIGNFELLWQPVVPPFSGSDLCVAGSVRRARRQVLPVCNLKASASLLDAQPLK 420  
QY 421 ARGPSAMPDPAQPPSPALQDRLGLKEEKGPLALLAPLRGAESGAAQPTRTKAAGKV 480  
Db 421 ARGPSAMPDPAQPPSPALQDRLGLKEEKGPLALLAPLRGAESGAAQPTRTKAAGKV 480  
QY 481 ELPACPCRHHVDSQAPNTGVPVAPAKSWDPNQLN 514  
Db 481 ELPACPCRHHVDSQAPNTGVPVAPAKSWDPNQLN 514

RESULT 4  
US-10-635-977-13  
; Sequence 13, Application US/10635977  
; Publication No. US20040171131A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN  
; FILE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42  
; FILE REFERENCE: D0283A CIP  
; CURRENT APPLICATION NUMBER: US/10/635,977  
; CURRENT FILING DATE: 2003-08-07  
; PRIOR APPLICATION NUMBER: U.S. 60/394,725  
; PRIOR FILING DATE: 2002-07-09  
; PRIOR APPLICATION NUMBER: U.S. 10/615,659  
; PRIOR FILING DATE: 2003-07-09  
; NUMBER OF SEQ ID NOS: 103  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 13  
; LENGTH: 541  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-635-977-13

Query Match 95.0%; Score 514; DB 4; Length 541;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MASSILKVVVSHQSCSRSSKPRDREAGSDLSRRDADNAEAKRLGLPQLVDIAC	60
Db	1	MASSILKVVVSHQSCSRSSKPRDREAGSDLSRRDADNAEAKRLGLPQLVDIAC	60
QY	61	KVCQAVLGQLEHEDIDTSADAVEDLTEAEWEDLTQYYSLVHGDAFISNSRNYFSQCQAL	120
Db	61	KVCQAVLGQLEHEDIDTSADAVEDLTEAEWEDLTQYYSLVHGDAFISNSRNYFSQCQAL	120
QY	121	LNRIITSVNPQTDIDGLRNIIWIKPAAKSRGRDIVCMRVEEILELAADHPLSRDNKVV	180
Db	121	LNRIITSVNPQTDIDGLRNIIWIKPAAKSRGRDIVCMRVEEILELAADHPLSRDNKVV	180
QY	181	QXVETPLICTKDIQWFLVTDNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLN	240
Db	181	QXVETPLICTKDIQWFLVTDNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLN	240
QY	241	AVQKYLKNDVGRSPLLPANHMTSTRFQYLRQGRGAVGWSVIYPSMKKAIAHAMKVAQ	300
Db	241	AVQKYLKNDVGRSPLLPANHMTSTRFQYLRQGRGAVGWSVIYPSMKKAIAHAMKVAQ	300
QY	301	DHVEPRKNSFELYGADFLGRDPRPMLIEINSSPTMHPSTPVTQAQVQEDTIKVAVD	360
Db	301	DHVEPRKNSFELYGADFLGRDPRPMLIEINSSPTMHPSTPVTQAQVQEDTIKVAVD	360
QY	361	RSCDIGNFELLRQPVVPPPPSGSDLCVAGYSVRRARQVLPVCNLKASILLDAQPLK	420
Db	361	RSCDIGNFELLRQPVVPPPPSGSDLCVAGYSVRRARQVLPVCNLKASILLDAQPLK	420
QY	421	ARGPSAMPDPAQPPSPALORDLGLKEKGLPLALLAPLRGAESGGAQPTRTKAAGV	480
Db	421	ARGPSAMPDPAQPPSPALORDLGLKEKGLPLALLAPLRGAESGGAQPTRTKAAGV	480
QY	481	ELPACPCRHVDSQAPNTGVPVQAQPAKSWDPNQLN	514
Db	481	ELPACPCRHVDSQAPNTGVPVQAQPAKSWDPNQLN	514

RESULT 5  
US-10-615-659-14  
; Sequence 14, Application US/10615659  
; Publication No. US20040157234A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN  
; FILE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42  
; FILE REFERENCE: D0283 NP

; CURRENT APPLICATION NUMBER: US/10/615,659  
; CURRENT FILING DATE: 2003-07-09  
; PRIOR APPLICATION NUMBER: U.S. 60/394,725  
; PRIOR FILING DATE: 2002-07-09  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 14  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-615-659-14

Query Match 54.2%; Score 293; DB 4; Length 293;  
Best Local Similarity 100.0%; Pred. No. 6.4e-287;  
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	73	EDIDTSADAVEDLTEAEWEDLTQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTD	132
Db	1	EDIDTSADAVEDLTEAEWEDLTQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTD	60
QY	133	IDGLRNIIWIKPAAKSRGRDIVCMRVEEILELAADHPLSRDNKVVQKYIETPLICD	192
Db	61	IDGLRNIIWIKPAAKSRGRDIVCMRVEEILELAADHPLSRDNKVVQKYIETPLICD	120
QY	193	TKFDIQRQWFLVTDNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLNNAVQKYLKNDVGR	252
Db	121	TKFDIQRQWFLVTDNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLNNAVQKYLKNDVGR	180
QY	253	SPLLPANHMTSTRFQYLRQGRGAVGWSVIYPSMKKAIAHAMKVAODHVEPRKNSFEL	312
Db	181	SPLLPANHMTSTRFQYLRQGRGAVGWSVIYPSMKKAIAHAMKVAODHVEPRKNSFEL	240
QY	313	YGADFLGRDPRPMLIEINSSPTMHPSTPVTQAQVQEDTIKVAVDSCDI	365
Db	241	YGADFLGRDPRPMLIEINSSPTMHPSTPVTQAQVQEDTIKVAVDSCDI	293

RESULT 6  
US-10-635-977-14  
; Sequence 14, Application US/10635977  
; Publication No. US20040171131A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN  
; FILE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42  
; FILE REFERENCE: D0283A CIP  
; CURRENT APPLICATION NUMBER: US/10/635,977  
; CURRENT FILING DATE: 2003-08-07  
; PRIOR APPLICATION NUMBER: U.S. 60/394,725  
; PRIOR FILING DATE: 2002-07-09  
; PRIOR APPLICATION NUMBER: U.S. 10/615,659  
; PRIOR FILING DATE: 2003-07-09  
; NUMBER OF SEQ ID NOS: 103  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 14  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-635-977-14

Query Match 54.2%; Score 293; DB 4; Length 293;  
Best Local Similarity 100.0%; Pred. No. 6.4e-287;  
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	73	EDIDTSADAVEDLTEAEWEDLTQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTD	132
Db	1	EDIDTSADAVEDLTEAEWEDLTQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTD	60
QY	133	IDGLRNIIWIKPAAKSRGRDIVCMRVEEILELAADHPLSRDNKVVQKYIETPLICD	192
Db	61	IDGLRNIIWIKPAAKSRGRDIVCMRVEEILELAADHPLSRDNKVVQKYIETPLICD	120
QY	193	TKFDIQRQWFLVTDNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLNNAVQKYLKNDVGR	252

Db 121 TKFDIRQWFLVTDWNPPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCCNNAVQKYLKNDVGR 180  
QY 253 SPLLPAHNMTSTRFOEYLQROGRGAVGWSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL 312  
Db 181 SPLLPAHNMTSTRFOEYLQROGRGAVGWSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL 240  
QY 313 YGADFVLGRDPRFWLIEINSSPTMHPSTPTVTAQLCAQVQEDTIKVAVDRSCDI 365  
Db 241 YGADFVLGRDPRFWLIEINSSPTMHPSTPTVTAQLCAQVQEDTIKVAVDRSCDI 293

RESULT 7  
US-10-615-659-4  
; Sequence 4, Application US/10615659  
; Publication No. US20040157234A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN  
; TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42  
; FILE REFERENCE: D0283 NP  
; CURRENT APPLICATION NUMBER: US/10/615,659  
; CURRENT FILING DATE: 2003-07-09  
; PRIOR APPLICATION NUMBER: U.S. 60/394,725  
; PRIOR FILING DATE: 2002-07-09  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 242  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-615-659-4

Query Match 44.7%; Score 242; DB 4; Length 242;  
Best Local Similarity 100.0%; Pred. No. 1.9e-235;  
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 133 IDGLRNIIWKPAKSRGRDIVCMRDEVEILELAADHPLSRDKNKVVQKYLTIETPLLICD 192  
Db 1 IDGLRNIIWKPAKSRGRDIVCMRDEVEILELAADHPLSRDKNKVVQKYLTIETPLLICD 60  
QY 193 TKFDIRQWFLVTDWNPPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCCNNAVQKYLKNDVGR 252  
Db 61 TKFDIRQWFLVTDWNPPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCCNNAVQKYLKNDVGR 120  
QY 253 SPLLPAHNMTSTRFOEYLQROGRGAVGWSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL 312  
Db 121 SPLLPAHNMTSTRFOEYLQROGRGAVGWSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL 180  
QY 313 YGADFVLGRDPRFWLIEINSSPTMHPSTPTVTAQLCAQVQEDTIKVAVDRSCDI 372  
Db 181 YGADFVLGRDPRFWLIEINSSPTMHPSTPTVTAQLCAQVQEDTIKVAVDRSCDI 240  
QY 373 RQ 374  
Db 241 RQ 242

RESULT 8  
US-10-635-977-4  
; Sequence 4, Application US/10635977  
; Publication No. US20040171131A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN  
; TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42  
; FILE REFERENCE: D0283A CIP  
; CURRENT APPLICATION NUMBER: US/10/635,977  
; CURRENT FILING DATE: 2003-08-07  
; PRIOR APPLICATION NUMBER: U.S. 60/394,725  
; PRIOR FILING DATE: 2002-07-09  
; PRIOR APPLICATION NUMBER: U.S. 10/615,659  
; PRIOR FILING DATE: 2003-07-09

; NUMBER OF SEQ ID NOS: 103  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 242  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-635-977-4  
Query Match 44.7%; Score 242; DB 4; Length 242;  
Best Local Similarity 100.0%; Pred. No. 1.9e-235;  
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 133 IDGLRNIIWKPAKSRGRDIVCMRDEVEILELAADHPLSRDKNKVVQKYLTIETPLLICD 192  
Db 1 IDGLRNIIWKPAKSRGRDIVCMRDEVEILELAADHPLSRDKNKVVQKYLTIETPLLICD 60  
QY 193 TKFDIRQWFLVTDWNPPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCCNNAVQKYLKNDVGR 252  
Db 61 TKFDIRQWFLVTDWNPPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCCNNAVQKYLKNDVGR 120  
QY 253 SPLLPAHNMTSTRFOEYLQROGRGAVGWSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL 312  
Db 121 SPLLPAHNMTSTRFOEYLQROGRGAVGWSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL 180  
QY 313 YGADFVLGRDPRFWLIEINSSPTMHPSTPTVTAQLCAQVQEDTIKVAVDRSCDI 372  
Db 181 YGADFVLGRDPRFWLIEINSSPTMHPSTPTVTAQLCAQVQEDTIKVAVDRSCDI 240  
QY 373 RQ 374  
Db 241 RQ 242

RESULT 9  
US-10-615-659-21  
; Sequence 21, Application US/10615659  
; Publication No. US20040157234A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN  
; TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42  
; FILE REFERENCE: D0283 NP  
; CURRENT APPLICATION NUMBER: US/10/615,659  
; CURRENT FILING DATE: 2003-07-09  
; PRIOR APPLICATION NUMBER: U.S. 60/394,725  
; PRIOR FILING DATE: 2002-07-09  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 21  
; LENGTH: 49  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-615-659-21

Query Match 9.1%; Score 49; DB 4; Length 49;  
Best Local Similarity 100.0%; Pred. No. 4.8e-41;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 192 DTKFDIRQWFLVTDWNPPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCCN 240  
Db 1 DTKFDIRQWFLVTDWNPPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCCN 49

RESULT 10  
US-10-615-659-22  
; Sequence 22, Application US/10615659  
; Publication No. US20040157234A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN  
; TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42  
; FILE REFERENCE: D0283 NP  
; CURRENT APPLICATION NUMBER: US/10/615,659

;/ CURRENT FILING DATE: 2003-07-09  
;/ PRIOR APPLICATION NUMBER: U.S. 60/394,725  
;/ PRIOR FILING DATE: 2002-07-09  
;/ NUMBER OF SEQ ID NOS: 102  
;/ SOFTWARE: PatentIn version 3.2  
;/ SEQ ID NO 22  
;/ LENGTH: 49  
;/ TYPE: PRT  
;/ ORGANISM: Rattus norvegicus  
US-10-615-659-22

Query Match 9.1%; Score 49; DB 4; Length 49;  
Best Local Similarity 100.0%; Pred. No. 4.8e-41;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 192 DTKFDIRQWFLVTDWNPNTIWFYKESYLRFSRSTQRFSLDKLDSAIHLCNN 240  
Db 1 DTKFDIRQWFLVTDWNPNTIWFYKESYLRFSRSTQRFSLDKLDSAIHLCNN 49

RESULT 11  
US-10-635-977-21  
;/ Sequence 21, Application US/10635977  
;/ Publication No. US20040171131A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Bristol-Myers Squibb Company  
;/ TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN  
;/ TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42  
;/ FILE REFERENCE: D0283A CIP  
;/ CURRENT APPLICATION NUMBER: US/10/635,977  
;/ CURRENT FILING DATE: 2003-08-07  
;/ PRIOR APPLICATION NUMBER: U.S. 60/394,725  
;/ PRIOR FILING DATE: 2002-07-09  
;/ PRIOR APPLICATION NUMBER: U.S. 10/615,659  
;/ PRIOR FILING DATE: 2003-07-09  
;/ NUMBER OF SEQ ID NOS: 103  
;/ SOFTWARE: PatentIn version 3.2  
;/ SEQ ID NO 21  
;/ LENGTH: 49  
;/ TYPE: PRT  
;/ ORGANISM: Mus musculus  
US-10-635-977-21

Query Match 9.1%; Score 49; DB 4; Length 49;  
Best Local Similarity 100.0%; Pred. No. 4.8e-41;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 192 DTKFDIRQWFLVTDWNPNTIWFYKESYLRFSRSTQRFSLDKLDSAIHLCNN 240  
Db 1 DTKFDIRQWFLVTDWNPNTIWFYKESYLRFSRSTQRFSLDKLDSAIHLCNN 49

RESULT 12  
US-10-635-977-22  
;/ Sequence 22, Application US/10635977  
;/ Publication No. US20040171131A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Bristol-Myers Squibb Company  
;/ TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN  
;/ TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42  
;/ FILE REFERENCE: D0283A CIP  
;/ CURRENT APPLICATION NUMBER: US/10/635,977  
;/ CURRENT FILING DATE: 2003-08-07  
;/ PRIOR APPLICATION NUMBER: U.S. 60/394,725  
;/ PRIOR FILING DATE: 2002-07-09  
;/ PRIOR APPLICATION NUMBER: U.S. 10/615,659  
;/ PRIOR FILING DATE: 2003-07-09  
;/ NUMBER OF SEQ ID NOS: 103  
;/ SOFTWARE: PatentIn version 3.2  
;/ SEQ ID NO 22  
;/ LENGTH: 49  
;/ TYPE: PRT  
;/ ORGANISM: Rattus norvegicus

US-10-635-977-22

Query Match 9.1%; Score 49; DB 4; Length 49;  
Best Local Similarity 100.0%; Pred. No. 4.8e-41;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 192 DTKFDIRQWFLVTDWNPNTIWFYKESYLRFSRSTQRFSLDKLDSAIHLCNN 240  
Db 1 DTKFDIRQWFLVTDWNPNTIWFYKESYLRFSRSTQRFSLDKLDSAIHLCNN 49

RESULT 13  
US-10-615-659-24  
;/ Sequence 24, Application US/10615659  
;/ Publication No. US20040157234A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Bristol-Myers Squibb Company  
;/ TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN  
;/ TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42  
;/ FILE REFERENCE: D0283 NP  
;/ CURRENT APPLICATION NUMBER: US/10/615,659  
;/ CURRENT FILING DATE: 2003-07-09  
;/ PRIOR APPLICATION NUMBER: U.S. 60/394,725  
;/ PRIOR FILING DATE: 2002-07-09  
;/ NUMBER OF SEQ ID NOS: 102  
;/ SOFTWARE: PatentIn version 3.2  
;/ SEQ ID NO 24  
;/ LENGTH: 42  
;/ TYPE: PRT  
;/ ORGANISM: Homo sapiens  
US-10-615-659-24

Query Match 7.8%; Score 42; DB 4; Length 42;  
Best Local Similarity 100.0%; Pred. No. 5e-34;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 482 LPACPCRHVDSQAPNTGVPAQPAKSWDPNQLNAHPLEPVL 523  
Db 1 LPACPCRHVDSQAPNTGVPAQPAKSWDPNQLNAHPLEPVL 42

RESULT 14  
US-10-635-977-24  
;/ Sequence 24, Application US/10635977  
;/ Publication No. US20040171131A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Bristol-Myers Squibb Company  
;/ TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN  
;/ TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42  
;/ FILE REFERENCE: D0283A CIP  
;/ CURRENT APPLICATION NUMBER: US/10/635,977  
;/ CURRENT FILING DATE: 2003-08-07  
;/ PRIOR APPLICATION NUMBER: U.S. 60/394,725  
;/ PRIOR FILING DATE: 2002-07-09  
;/ PRIOR APPLICATION NUMBER: U.S. 10/615,659  
;/ PRIOR FILING DATE: 2003-07-09  
;/ NUMBER OF SEQ ID NOS: 103  
;/ SOFTWARE: PatentIn version 3.2  
;/ SEQ ID NO 24  
;/ LENGTH: 42  
;/ TYPE: PRT  
;/ ORGANISM: Homo sapiens  
US-10-635-977-24

Query Match 7.8%; Score 42; DB 4; Length 42;  
Best Local Similarity 100.0%; Pred. No. 5e-34;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 482 LPACPCRHVDSQAPNTGVPAQPAKSWDPNQLNAHPLEPVL 523  
Db 1 LPACPCRHVDSQAPNTGVPAQPAKSWDPNQLNAHPLEPVL 42

```
RESULT 15
US-10-615-659-23
; Sequence 23, Application US/10615659
; Publication No. US20040157234A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
; FILE REFERENCE: D0283 NP
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/10/615,659
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: U.S. 60/394,725
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-615-659-23

Query Match      4.8%; Score 26; DB 4; Length 26;
Best Local Similarity 100.0%; Pred.No. 4.7e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      332 SSPTMHPSTPVTATQLCAQVOEDTIKV 357
Db      1 SSPTMHPSTPVTATQLCAQVOEDTIKV 26
```

Search completed: May 15, 2006, 09:59:56  
Job time : 85 secs



GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2006, 09:57:49 ; Search time 27 Seconds  
(without alignments)  
1656.576 Million cell updates/sec

Title: US-10-635-977-2  
Perfect score: 541  
Sequence: 1 MASSILKVVVSHQSCSRSSR.....LRLKTAEGALRPPPGKGS 541

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 1

Total number of hits satisfying chosen parameters: 570988

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents\_AA:\*  
1: /cgn2\_6/prodata/1/iaa/5 COMB.pep.\*  
2: /cgn2\_6/prodata/1/iaa/6 COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/H COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/PCUTUS COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/RE COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	1.5	96	2 US-09-220-528-19	Sequence 19, Appl
2	8	1.5	96	2 US-09-473-551-9	Sequence 9, Appl
3	8	1.5	113	2 US-09-220-528-3	Sequence 3, Appl
4	8	1.5	113	2 US-09-347-613C-7	Sequence 7, Appl
5	8	1.5	113	2 US-09-347-613C-12	Sequence 12, Appl
6	8	1.5	113	2 US-09-662-183A-7	Sequence 7, Appl
7	8	1.5	113	2 US-09-662-183A-12	Sequence 12, Appl
8	8	1.5	116	2 US-09-220-528-4	Sequence 4, Appl
9	8	1.5	116	2 US-09-347-613C-6	Sequence 6, Appl
10	8	1.5	116	2 US-09-347-613C-11	Sequence 11, Appl
11	8	1.5	116	2 US-09-662-183A-6	Sequence 6, Appl
12	8	1.5	116	2 US-09-662-183A-11	Sequence 11, Appl
13	8	1.5	140	2 US-09-220-528-5	Sequence 5, Appl
14	8	1.5	140	2 US-09-347-613C-5	Sequence 5, Appl
15	8	1.5	140	2 US-09-347-613C-10	Sequence 10, Appl
16	8	1.5	140	2 US-09-662-183A-5	Sequence 5, Appl
17	8	1.5	140	2 US-09-662-183A-10	Sequence 10, Appl
18	8	1.5	159	2 US-09-220-528-12	Sequence 12, Appl
19	8	1.5	159	2 US-09-220-528-89	Sequence 89, Appl
20	8	1.5	165	2 US-09-534-811-8	Sequence 8, Appl
21	8	1.5	181	2 US-09-220-528-40	Sequence 40, Appl
22	8	1.5	200	2 US-09-347-613C-2	Sequence 2, Appl
23	8	1.5	200	2 US-09-662-183A-2	Sequence 2, Appl
24	8	1.5	220	2 US-09-220-528-26	Sequence 26, Appl
25	8	1.5	220	2 US-09-347-613C-9	Sequence 9, Appl
26	8	1.5	220	2 US-09-347-613C-35	Sequence 35, Appl
27	8	1.5	220	2 US-09-662-183A-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1

US-09-220-528-19  
; Sequence 19, Application US/09220528A  
; Patent No. 6284540  
; GENERAL INFORMATION:  
; APPLICANT: Milbrandt, Jeffrey D.  
; TITLE OF INVENTION: Artemin, A No. 6284540el Neurotrophic Factor  
; FILE REFERENCE: 6029-7998  
; CURRENT APPLICATION NUMBER: US/09/220,528A  
; CURRENT FILING DATE: 1998-12-24  
; EARLIER APPLICATION NUMBER: 09/218,598  
; EARLIER FILING DATE: 1998-12-22  
; EARLIER APPLICATION NUMBER: 60/108,148  
; EARLIER FILING DATE: 1998-11-12  
; EARLIER APPLICATION NUMBER: 09/163,283  
; EARLIER FILING DATE: 1998-09-29  
; NUMBER OF SEQ ID NOS: 120  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 96  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-220-528-19

Query Match 1.5%; Score 8; DB 2; Length 96;  
Best Local Similarity 100.0%; Pred. No. 4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 530 GALTREPPG 537  
DB 50 GALTREPPG 57

RESULT 2

US-09-473-551-9  
; Sequence 9, Application US/09473551  
; Patent No. 6866851  
; GENERAL INFORMATION:  
; APPLICANT: Milbrandt, Jeffrey D.  
; APPLICANT: Baloh, Robert H.  
; TITLE OF INVENTION: GFR-alpha-1-RET Specific Agonists and Methods Therefor  
; FILE REFERENCE: 6029-9879  
; CURRENT APPLICATION NUMBER: US/09/473,551  
; CURRENT FILING DATE: 1999-12-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 96  
; TYPE: PRT

```
; ORGANISM: Homo sapiens
US-09-473-551-9

Query Match      1.5%; Score 8; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 4;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      530 GALRPPPG 537
Db      50 GALRPPPG 57

RESULT 3
US-09-220-528-3
; Sequence 3, Application US/09220528A
; Patent No. 6284540
; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey D.
; APPLICANT: Baloh, Robert H.
; TITLE OF INVENTION: Artemin, A No. 6284540el Neurotrophic Factor
; FILE REFERENCE: 6029-7998
; CURRENT APPLICATION NUMBER: US/09/220,528A
; CURRENT FILING DATE: 1998-12-24
; EARLIER APPLICATION NUMBER: 09/218,698
; EARLIER FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/108,148
; EARLIER FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: 09/163,283
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-220-528-3

Query Match      1.5%; Score 8; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      530 GALRPPPG 537
Db      65 GALRPPPG 72

RESULT 4
US-09-347-613C-7
; Sequence 7, Application US/09347613C
; Patent No. 6593133
; GENERAL INFORMATION:
; APPLICANT: Johansen, Teit E.
; APPLICANT: Blom, Nikolaj
; APPLICANT: Hansen, Claus
; TITLE OF INVENTION: No. 6593133el Neurotrophic Factors
; FILE REFERENCE: NeuroSearch 19313-001
; CURRENT APPLICATION NUMBER: US/09/347,613C
; CURRENT FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: DANISH 1998 00904
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: USSN 60/092,229
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: DANISH 1998 01048
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: USSN 60/097,774
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: DANISH 1998 01260
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: USSN 60/103,908
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: DANISH 1998 01265
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-347-613C-7

Query Match      1.5%; Score 8; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      530 GALRPPPG 537
Db      65 GALRPPPG 72

RESULT 5
US-09-347-613C-12
; Sequence 12, Application US/09347613C
; Patent No. 6593133
; GENERAL INFORMATION:
; APPLICANT: Johansen, Teit E.
; APPLICANT: Blom, Nikolaj
; APPLICANT: Hansen, Claus
; TITLE OF INVENTION: No. 6593133el Neurotrophic Factors
; FILE REFERENCE: NeuroSearch 19313-001
; CURRENT APPLICATION NUMBER: US/09/347,613C
; CURRENT FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: DANISH 1998 00904
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: USSN 60/092,229
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: DANISH 1998 01048
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: USSN 60/097,774
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: DANISH 1998 01260
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: USSN 60/103,908
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: DANISH 1998 01265
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-347-613C-12

Query Match      1.5%; Score 8; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      530 GALRPPPG 537
Db      65 GALRPPPG 72

RESULT 6
US-09-662-183A-7
```

; Sequence 7, Application US/09662183A  
; Patent No. 6734284  
; GENERAL INFORMATION:  
; APPLICANT: Johansen, Teit E.  
; APPLICANT: Blom, Nikolaj  
; APPLICANT: Hansen, Claus  
; TITLE OF INVENTION: No. 6734284el Neurotrophic Factors  
; FILE REFERENCE: 19313-001 DIV  
; CURRENT APPLICATION NUMBER: US/09/662,183A  
; CURRENT FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: DANISH 1998 00904  
; PRIOR FILING DATE: 1998-07-06  
; PRIOR APPLICATION NUMBER: USSN 60/092,229  
; PRIOR FILING DATE: 1998-07-09  
; PRIOR APPLICATION NUMBER: DANISH 1998 01048  
; PRIOR FILING DATE: 1998-08-19  
; PRIOR APPLICATION NUMBER: USSN 60/097,774  
; PRIOR FILING DATE: 1998-08-25  
; PRIOR APPLICATION NUMBER: DANISH 1998 01260  
; PRIOR FILING DATE: 1998-10-05  
; PRIOR APPLICATION NUMBER: USSN 60/103,908  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: DANISH 1998 01265  
; PRIOR FILING DATE: 1998-10-06  
; PRIOR APPLICATION NUMBER: 09/347,613  
; PRIOR FILING DATE: 2000-07-02  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (107)  
; OTHER INFORMATION: Wherein Xaa at position 107 designates Asn or Thr  
; LOCATION: (108)  
; NAME/KEY: VARIANT  
; OTHER INFORMATION: Wherein Xaa at position 108 designates Ala or Pro  
US-09-662-183A-7

Query Match 1.5%; Score 8; DB 2; Length 113;  
Best Local Similarity 100.0%; Pred. No. 4.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 530 GALRPPPG 537  
| | | | |  
Db 65 GALRPPPG 72

RESULT 7  
US-09-662-183A-12  
; Sequence 12, Application US/09662183A  
; Patent No. 6734284  
; GENERAL INFORMATION:  
; APPLICANT: Johansen, Teit E.  
; APPLICANT: Blom, Nikolaj  
; APPLICANT: Hansen, Claus  
; TITLE OF INVENTION: No. 6734284el Neurotrophic Factors  
; FILE REFERENCE: 19313-001 DIV  
; CURRENT APPLICATION NUMBER: US/09/662,183A  
; CURRENT FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: DANISH 1998 00904  
; PRIOR FILING DATE: 1998-07-06  
; PRIOR APPLICATION NUMBER: USSN 60/092,229  
; PRIOR FILING DATE: 1998-07-09  
; PRIOR APPLICATION NUMBER: DANISH 1998 01048  
; PRIOR FILING DATE: 1998-08-19  
; PRIOR APPLICATION NUMBER: USSN 60/097,774  
; PRIOR FILING DATE: 1998-08-25  
; PRIOR APPLICATION NUMBER: DANISH 1998 01260  
; PRIOR FILING DATE: 1998-10-05

; PRIOR APPLICATION NUMBER: USSN 60/103,908  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: DANISH 1998 01265  
; PRIOR FILING DATE: 1998-10-06  
; PRIOR APPLICATION NUMBER: 09/347,613  
; PRIOR FILING DATE: 2000-07-02  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CARBOHYD  
; LOCATION: (95)  
; OTHER INFORMATION: glycosylated asparagine  
US-09-662-183A-12

Query Match 1.5%; Score 8; DB 2; Length 113;  
Best Local Similarity 100.0%; Pred. No. 4.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 530 GALRPPPG 537  
| | | | |  
Db 65 GALRPPPG 72

RESULT 8  
US-09-220-528-4  
; Sequence 4, Application US/09220528A  
; Patent No. 6284540  
; GENERAL INFORMATION:  
; APPLICANT: Milbrandt, Jeffrey D.  
; APPLICANT: Baloh, Robert H.  
; TITLE OF INVENTION: Artemin, A No. 6284540el Neurotrophic Factor  
; FILE REFERENCE: 6029-1998  
; CURRENT APPLICATION NUMBER: US/09/220,528A  
; CURRENT FILING DATE: 1998-12-24  
; EARLIER APPLICATION NUMBER: 09/218,698  
; EARLIER FILING DATE: 1998-12-22  
; EARLIER APPLICATION NUMBER: 60/108,148  
; EARLIER FILING DATE: 1998-11-12  
; EARLIER APPLICATION NUMBER: 09/163,283  
; EARLIER FILING DATE: 1998-09-29  
; NUMBER OF SEQ ID NOS: 120  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-220-528-4

Query Match 1.5%; Score 8; DB 2; Length 116;  
Best Local Similarity 100.0%; Pred. No. 4.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 530 GALRPPPG 537  
| | | | |  
Db 68 GALRPPPG 75

RESULT 9  
US-09-347-613C-6  
; Sequence 6, Application US/09347613C  
; Patent No. 6593133  
; GENERAL INFORMATION:  
; APPLICANT: Johansen, Teit E.  
; APPLICANT: Blom, Nikolaj  
; APPLICANT: Hansen, Claus  
; TITLE OF INVENTION: No. 6593133el Neurotrophic Factors  
; FILE REFERENCE: Neurosearch 19313-001  
; CURRENT APPLICATION NUMBER: US/09/347,613C  
; CURRENT FILING DATE: 1999-07-02

```
; PRIOR APPLICATION NUMBER: DANISH 1998 00904
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: USSN 60/092,229
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: DANISH 1998 01048
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: USSN 60/097,774
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: DANISH 1998 01260
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: USSN 60/103,908
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: DANISH 1998 01265
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (110)
; OTHER INFORMATION: Wherein Xaa at position 110 designates Asn or Thr
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (111)
; OTHER INFORMATION: Wherein Xaa at position 111 designates Ala or Pro
; US-09-347-613C-6
Query Match 1.5%; Score 8; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 530 GALTTPPG 537
Db 68 GALTTPPG 75
RESULT 10
US-09-347-613C-11
; Sequence 11, Application US/09347613C
; Patent No. 6593133
; GENERAL INFORMATION:
; APPLICANT: Johansen, Teit E.
; APPLICANT: Blom, Nikolaj
; TITLE OF INVENTION: No. 6593133el Neurotrophic Factors
; FILE REFERENCE: NeuroSearch 19313-001
; CURRENT APPLICATION NUMBER: US/09/347,613C
; CURRENT FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: DANISH 1998 00904
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: USSN 60/092,229
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: DANISH 1998 01048
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: USSN 60/097,774
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: DANISH 1998 01260
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: DANISH 1998 01265
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (110)
; OTHER INFORMATION: Wherein Xaa at position 110 designates Asn or Thr
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (111)
; OTHER INFORMATION: Wherein Xaa at position 111 designates Ala or Pro
; US-09-347-613C-6
Query Match 1.5%; Score 8; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 530 GALTTPPG 537
Db 68 GALTTPPG 75
RESULT 11
US-09-662-183A-6
; Sequence 6, Application US/09662183A
; Patent No. 6734284
; GENERAL INFORMATION:
; APPLICANT: Johansen, Teit E.
; APPLICANT: Blom, Nikolaj
; TITLE OF INVENTION: No. 6734284el Neurotrophic Factors
; FILE REFERENCE: 19313-001 DIV
; CURRENT APPLICATION NUMBER: US/09/662,183A
; CURRENT FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: DANISH 1998 00904
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: USSN 60/092,229
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: DANISH 1998 01048
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: USSN 60/097,774
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: DANISH 1998 01260
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: USSN 60/103,908
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: DANISH 1998 01265
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 09/347,613
; PRIOR FILING DATE: 2000-07-02
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (110)
; OTHER INFORMATION: Wherein Xaa at position 110 designates Asn or Thr
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (111)
; OTHER INFORMATION: Wherein Xaa at position 111 designates Ala or Pro
; US-09-662-183A-6
Query Match 1.5%; Score 8; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 530 GALTTPPG 537
Db 68 GALTTPPG 75
RESULT 12
US-09-662-183A-11
; Sequence 11, Application US/09662183A
; Patent No. 6734284
; GENERAL INFORMATION:
; APPLICANT: Johansen, Teit E.
; APPLICANT: Blom, Nikolaj
```

```
; LOCATION: (98)
; OTHER INFORMATION: glycosylated asparagine
; US-09-347-613C-11
Query Match 1.5%; Score 8; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 530 GALTTPPG 537
Db 68 GALTTPPG 75
RESULT 11
US-09-662-183A-6
; Sequence 6, Application US/09662183A
; Patent No. 6734284
; GENERAL INFORMATION:
; APPLICANT: Johansen, Teit E.
; APPLICANT: Blom, Nikolaj
; TITLE OF INVENTION: No. 6734284el Neurotrophic Factors
; FILE REFERENCE: 19313-001 DIV
; CURRENT APPLICATION NUMBER: US/09/662,183A
; CURRENT FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: DANISH 1998 00904
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: USSN 60/092,229
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: DANISH 1998 01048
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: USSN 60/097,774
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: DANISH 1998 01260
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: USSN 60/103,908
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: DANISH 1998 01265
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 09/347,613
; PRIOR FILING DATE: 2000-07-02
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (110)
; OTHER INFORMATION: Wherein Xaa at position 110 designates Asn or Thr
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (111)
; OTHER INFORMATION: Wherein Xaa at position 111 designates Ala or Pro
; US-09-662-183A-6
Query Match 1.5%; Score 8; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 530 GALTTPPG 537
Db 68 GALTTPPG 75
RESULT 12
US-09-662-183A-11
; Sequence 11, Application US/09662183A
; Patent No. 6734284
; GENERAL INFORMATION:
; APPLICANT: Johansen, Teit E.
; APPLICANT: Blom, Nikolaj
```

APPLICANT: Hansen, Claus  
; TITLE OF INVENTION: No. 6734284e1 Neurotrophic Factors  
; FILE REFERENCE: 19313-001 DIV  
; CURRENT APPLICATION NUMBER: US/09/662,183A  
; CURRENT FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: DANISH 1998 00904  
; PRIOR FILING DATE: 1998-07-06  
; PRIOR APPLICATION NUMBER: USSN 60/092,229  
; PRIOR FILING DATE: 1998-07-09  
; PRIOR APPLICATION NUMBER: DANISH 1998 01048  
; PRIOR FILING DATE: 1998-08-19  
; PRIOR APPLICATION NUMBER: USSN 60/097,774  
; PRIOR FILING DATE: 1998-08-25  
; PRIOR APPLICATION NUMBER: DANISH 1998 01260  
; PRIOR FILING DATE: 1998-10-05  
; PRIOR APPLICATION NUMBER: USSN 60/103,908  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: DANISH 1998 01265  
; PRIOR FILING DATE: 1998-10-06  
; PRIOR APPLICATION NUMBER: 09/347,613  
; PRIOR FILING DATE: 2000-07-02  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CARBOHYD  
; LOCATION: (98)  
; OTHER INFORMATION: glycosylated asparagine  
US-09-662-183A-11

Query Match 1.5%; Score 8; DB 2; Length 116;  
Best Local Similarity 100.0%; Pred. No. 4.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 530 GALRPPPG 537  
|||||||  
Db 68 GALRPPPG 75

RESULT 13  
US-09-220-528-5  
; Sequence 5, Application US/09220528A  
; Patent No. 6284540  
; GENERAL INFORMATION:  
; APPLICANT: Milbrandt, Jeffrey D.  
; TITLE OF INVENTION: Artemin, A No. 6284540e1 Neurotrophic Factor  
; FILE REFERENCE: 6029-7998  
; CURRENT APPLICATION NUMBER: US/09/220,528A  
; CURRENT FILING DATE: 1998-12-24  
; EARLIER APPLICATION NUMBER: 09/218,698  
; EARLIER FILING DATE: 1998-12-22  
; EARLIER APPLICATION NUMBER: 60/108,148  
; EARLIER FILING DATE: 1998-11-12  
; EARLIER APPLICATION NUMBER: 09/163,283  
; EARLIER FILING DATE: 1998-09-29  
; NUMBER OF SEQ ID NOS: 120  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 140  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-220-528-5

Query Match 1.5%; Score 8; DB 2; Length 140;  
Best Local Similarity 100.0%; Pred. No. 5.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 530 GALRPPPG 537  
|||||||

Db 92 GALRPPPG 99  
RESULT 14  
US-09-347-613C-5  
; Sequence 5, Application US/09347613C  
; Patent No. 6593133  
; GENERAL INFORMATION:  
; APPLICANT: Johansen, Teit E.  
; APPLICANT: Blom, Nikolaj  
; APPLICANT: Hansen, Claus  
; TITLE OF INVENTION: No. 6593133e1 Neurotrophic Factors  
; FILE REFERENCE: NeuroSearch 19313-001  
; CURRENT APPLICATION NUMBER: US/09/347,613C  
; CURRENT FILING DATE: 1999-07-02  
; PRIOR APPLICATION NUMBER: DANISH 1998 00904  
; PRIOR FILING DATE: 1998-07-06  
; PRIOR APPLICATION NUMBER: USSN 60/092,229  
; PRIOR FILING DATE: 1998-07-09  
; PRIOR APPLICATION NUMBER: DANISH 1998 01048  
; PRIOR FILING DATE: 1998-08-19  
; PRIOR APPLICATION NUMBER: USSN 60/097,774  
; PRIOR FILING DATE: 1998-08-25  
; PRIOR APPLICATION NUMBER: DANISH 1998 01260  
; PRIOR FILING DATE: 1998-10-05  
; PRIOR APPLICATION NUMBER: USSN 60/103,908  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: DANISH 1998 01265  
; PRIOR FILING DATE: 1998-10-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 140  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (134)  
; OTHER INFORMATION: Wherein Xaa at position 134 designates Asn or Thr  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (135)  
; OTHER INFORMATION: Wherein Xaa at position 135 designates Ala or Pro  
US-09-347-613C-5

Query Match 1.5%; Score 8; DB 2; Length 140;  
Best Local Similarity 100.0%; Pred. No. 5.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 530 GALRPPPG 537  
|||||||  
Db 92 GALRPPPG 99

RESULT 15  
US-09-347-613C-10  
; Sequence 10, Application US/09347613C  
; Patent No. 6593133  
; GENERAL INFORMATION:  
; APPLICANT: Johansen, Teit E.  
; APPLICANT: Blom, Nikolaj  
; APPLICANT: Hansen, Claus  
; TITLE OF INVENTION: No. 6593133e1 Neurotrophic Factors  
; FILE REFERENCE: NeuroSearch 19313-001  
; CURRENT APPLICATION NUMBER: US/09/347,613C  
; CURRENT FILING DATE: 1999-07-02  
; PRIOR APPLICATION NUMBER: DANISH 1998 00904  
; PRIOR FILING DATE: 1998-07-06  
; PRIOR APPLICATION NUMBER: USSN 60/092,229  
; PRIOR FILING DATE: 1998-07-09  
; PRIOR APPLICATION NUMBER: DANISH 1998 01048  
; PRIOR FILING DATE: 1998-08-19  
; PRIOR APPLICATION NUMBER: USSN 60/097,774

QY 530 GALRPPPG 537  
|||||||

```
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: DANISH 1998 01260
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: USSN 60/103,908
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: DANISH 1998 01265
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (122)
; OTHER INFORMATION: glycosylated asparagine
US-09-347-613C-10

Query Match      1.5%; Score 8; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 530 GALLRPPPG 537
Db 92 GALLRPPPG 99

Search completed: May 15, 2006, 09:58:24
Job time : 27 secs
```

GenCore version 5.1.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2006, 09:56:28 ; Search time 62 Seconds  
(without alignments)  
3833.934 Million cell updates/sec

Title: US-10-635-977-2

Perfect score: 541

Sequence: 1 MASSILKVVSHQSCSRSSR.....LRGLKTABGALRPPPGKGS 541

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2442881

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- A\_Geneseq\_21.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

length of watch

Result No.	Score	Query Match	Length	DB ID	Description
1	541	100.0	541	8	Adj93358 Human BGS
2	514	95.0	541	8	Adj93365 Human tub
3	293	54.2	293	8	Adj93366 Human BGS
4	242	44.7	242	8	Adj93360 Human BGS
5	101	18.7	402	8	Adu02747 Novel hum
6	49	9.1	49	8	Adj93373 Human BGS
7	42	7.8	42	8	Adj93376 Human BGS
8	39	7.2	61	8	Adj93452 Human BGS
9	26	4.8	26	8	Adj93374 Human BGS
10	23	4.3	23	8	Adj93371 Human BGS
11	17	3.1	17	8	Adj93377 Human BGS
12	16	3.0	16	8	Adj93397 Human BGS
13	16	3.0	16	8	Adj93398 Human BGS
14	16	3.0	16	8	Adj93401 Human BGS
15	16	3.0	16	8	Adj93396 Human BGS
16	16	3.0	16	8	Adj93400 Human BGS
17	16	3.0	16	8	Adj93399 Human BGS
18	14	2.6	14	8	Adj93390 Human BGS
19	14	2.6	14	8	Adj93389 Human BGS
20	14	2.6	14	8	Adj93394 Human BGS
21	14	2.6	14	8	Adj93393 Human BGS
22	14	2.6	14	8	Adj93388 Human BGS
23	14	2.6	14	8	Adj93392 Human BGS
24	14	2.6	14	8	Adj93395 Human BGS

25	14	2.6	14	8	ADJ933391	Adj933391 Human BGS
26	13	2.4	13	8	ADJ933383	Adj933383 Human BGS
27	13	2.4	13	8	ADJ933387	Adj933387 Human BGS
28	13	2.4	13	8	ADJ933368	Adj933368 Human BGS
29	13	2.4	13	8	ADJ933386	Adj933386 Human BGS
30	13	2.4	13	8	ADJ933382	Adj933382 Human BGS
31	13	2.4	13	8	ADJ933384	Adj933384 Human BGS
32	13	2.4	13	8	ADJ933375	Adj933375 Human BGS
33	13	2.4	13	8	ADJ933385	Adj933385 Human BGS
34	13	2.4	13	8	ADJ933372	Adj933372 Human BGS
35	13	2.4	13	8	ADJ933381	Adj933381 Human BGS
36	13	2.4	292	8	ADJ93455	Adj93455 Human HOT
37	13	2.4	326	7	ADM05524	Adm05524 Human pro
38	13	2.4	352	3	AAB43005	Aab43005 Human ORF
39	13	2.4	352	4	AAM39450	Aam39450 Human pol
40	13	2.4	352	8	ADJ93457	Adj93457 Human HOT
41	13	2.4	352	8	ABM80420	Abm80420 Tumour-as
42	13	2.4	362	3	AAB58909	Aab58909 Breast an
43	13	2.4	362	4	AAM41236	Aam41236 Human pol
44	13	2.4	399	6	ABU11512	Abu11512 Human MDD
45	13	2.4	488	5	AAU74334	Aau74334 Human cyt

ALIGNMENTS

RESULT 1

ADJ933358  
ID ADJ933358 standard; protein; 541 AA.  
XX AC ADJ933358;  
XX DT 06-MAY-2004 (first entry)  
XX DE Human BGS-42 protein sequence SeqID2.  
XX KW testis-specific tubulin tyrosine-ligase-like polypeptide;  
KW BGS-42 polypeptide; cytotostatic; respiratory-Gen; gastrointestinal-Gen;  
KW neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive;  
KW osteopathic; nootropic; antiparkinsonian; antiarthritic; antiasthmatic;  
KW anti-HIV; antibacterial; immunosuppressive; antiseborrheic;  
KW dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;  
KW tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;  
KW testicular disorder; testicular cancer; pulmonary disorder; lung cancer;  
KW gastrointestinal disorder; colon cancer; stomach cancer; neural disorder;  
KW brain cancer; liver cancer; proliferative condition; testis; lung;  
KW small intestine; brain; lymph tissue; infertility; Cushing's syndrome;  
KW emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease;  
KW Parkinson's disease; immunological disorder; arthritis; asthma; AIDS;  
KW sepsis; acne; Sjogren's disease; scleroderma; human.  
Homo sapiens.  
WO2004005487-A2.  
15-JAN-2004.  
09-JUL-2003; 2003WO-US021605.  
09-JUL-2002; 2002US-0394725P.  
(BRIM ) BRISTOL-MYERS SQUIBB CO.  
Feder JN, Wu S, Nelson TC;  
WPI; 2004-099381/10.  
N-PSDB; ADJ933357.  
New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide,  
PT useful for preventing, treating or ameliorating a medical condition, e.g.  
PT aberrant cellular proliferation, reproductive disorders or testicular  
disorders.  
XX

PS Claim 5; SEQ ID NO 2; 343pp; English.

XX This invention relates to a novel testis-specific tubulin tyrosine-ligase-like polypeptide, designated the BGS-42 polypeptide. The invention may be useful for the development of compounds with a cytostatic, respiratory

CC -Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen, antiinflammatory, anabolic, hypertensive, osteopathic, neurotropic, antiparkinsonian, antiarthritic, antiasthmatic, anti-HIV, antibacterial, immunosuppressive, antiseborrheic or dermatological activity acting as tyrosine ligase modulators. In addition, the disclosed sequences may be useful for gene therapy. The BGS-42 polypeptide or polynucleotide can be used for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, and for preventing, treating or ameliorating a medical condition, such as a disorder related to aberrant tubulin ligase activity, a disorder related to aberrant tubulin-carboxypeptidase activity, aberrant cellular proliferation, reproductive disorders, testicular disorders, testicular cancer, pulmonary disorders, lung cancer, gastrointestinal disorders, colon cancer, stomach cancer, neural disorders, brain cancer, liver cancer, or proliferative condition of the testis, lung, small intestine, brain or lymph tissue. The BGS-42 polypeptide, polynucleotide, or their modulators are also useful for treating infertility, Cushing's syndrome, emphysema, Addison's disease, acromegaly, Alzheimer's disease, or Parkinson's disease. The BGS-42 polypeptide can be used as a preventive agent for immunological disorders including arthritis, asthma, AIDS, sepsis, acne, Sjogren's disease or scleroderma. The antibodies may be used to purify, detect and target the BGS-42 polypeptides. The present sequence is that of the human BGS-42 protein of the invention.

XX Sequence 541 AA;

Query Match 100.0%; Score 541; DB 8; Length 541;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASSILKVVVSHOSCRSSRSPKRDORERAGSSDLSSRQDAENAEAKRLGPLQVLDIAC 60

Db 1 MASSILKVVVSHOSCRSSRSPKRDORERAGSSDLSSRQDAENAEAKRLGPLQVLDIAC 60

QY 61 KVQAVYLQGLEHEDIDTSADAVEDLTEAEWEDLTQQYSLVHGDFAFISNRYFSQCQAL 120

Db 61 KVQAVYLQGLEHEDIDTSADAVEDLTEAEWEDLTQQYSLVHGDFAFISNRYFSQCQAL 120

QY 121 LNRITSVNPTDIDGLRNIIWIKPAKSRGRDIVCMRDVBEIELELAADHPLSRDNKVVV 180

Db 121 LNRITSVNPTDIDGLRNIIWIKPAKSRGRDIVCMRDVBEIELELAADHPLSRDNKVVV 180

QY 181 QKYIETPLLCDTKFDIROMFLVTDNNPLTIWFYKESYLFSTQRTSLDKLDSAIHLCNN 240

Db 181 QKYIETPLLCDTKFDIROMFLVTDNNPLTIWFYKESYLFSTQRTSLDKLDSAIHLCNN 240

QY 241 AVQKYLKNDVGRSPLLPAHNMTWISTRFOEYLQQRGAVMGSVIYPSMKKAI AHAMKVAQ 300

Db 241 AVQKYLKNDVGRSPLLPAHNMTWISTRFOEYLQQRGAVMGSVIYPSMKKAI AHAMKVAQ 300

QY 301 DHVEPRKNSFELYGADVFLGRDRFPWLIEINSSPTMHPSTPVTVAQLCAQVQEDTIKVAVD 360

Db 301 DHVEPRKNSFELYGADVFLGRDRFPWLIEINSSPTMHPSTPVTVAQLCAQVQEDTIKVAVD 360

QY 361 RSCDIGNFWLLWQPVVPEPPFGSSDLCVAGSVRRARROVLPVCNLIKASALLDQAQPLK 420

Db 361 RSCDIGNFWLLWQPVVPEPPFGSSDLCVAGSVRRARROVLPVCNLIKASALLDQAQPLK 420

QY 421 ARGPSAMPDPAQGPSPALQDLGLKEKGLPLALLAPLRGAABSGGAAQPTRTKAAGV 480

Db 421 ARGPSAMPDPAQGPSPALQDLGLKEKGLPLALLAPLRGAABSGGAAQPTRTKAAGV 480

QY 481 ELPACPCRHDVSQAPNTGVPAQPAKSWDPNQLNAHPLPVLRLKLTAEAGALRPPPGGKG 540

Db 481 ELPACPCRHDVSQAPNTGVPAQPAKSWDPNQLNAHPLPVLRLKLTAEAGALRPPPGGKG 540

QY 541 S 541

Db 541 S 541

RESULT 2

ADJ93365

ID ADJ93365 standard; protein; 541 AA.

XX ADJ93365;

AC ADJ93365;

XX 06-MAY-2004 (first entry)

XX Human tubulin tyrosine ligase protein consensus sequence SeqID13.

DE testis-specific tubulin tyrosine-ligase-like polypeptide;

XX BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen; neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive; osteopathic; neurotropic; antiparkinsonian; antiarthritic; antiasthmatic; anti-HIV; antibacterial; immunosuppressive; antiseborrheic; dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase; tubulin-carboxypeptidase; cellular proliferation; reproductive disorder; testicular disorder; testicular cancer; pulmonary disorder; lung cancer; gastrointestinal disorder; colon cancer; stomach cancer; neural disorder; brain cancer; liver cancer; proliferative condition; testis; lung; small intestine; brain; lymph tissue; infertility; Cushing's syndrome; emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease; Parkinson's disease; immunological disorder; arthritis; asthma; AIDS; sepsis; acne; Sjogren's disease; scleroderma; human.

XX Homo sapiens.

OS Synthetic.

XX WO2004005487-A2.

XX 15-JAN-2004.

XX 09-JUL-2003; 2003WO-US021605.

XX 09-JUL-2002; 2002US-0394725P.

XX (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX Feder JN, Wu S, Nelson TC;

XX WPI; 2004-099381/10.

DR N-PSDB; ADJ93364.

XX New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, e.g. aberrant cellular proliferation, reproductive disorders or testicular disorders.

PS Example 4; SEQ ID NO 13; 343pp; English.

XX This invention relates to a novel testis-specific tubulin tyrosine-ligase-like polypeptide, designated the BGS-42 polypeptide. The invention may be useful for the development of compounds with a cytostatic, respiratory

CC -Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen, antiinflammatory, anabolic, hypertensive, osteopathic, neurotropic, antiparkinsonian, antiarthritic, antiasthmatic, anti-HIV, antibacterial, immunosuppressive, antiseborrheic or dermatological activity acting as tyrosine ligase modulators. In addition, the disclosed sequences may be useful for gene therapy. The BGS-42 polypeptide or polynucleotide can be used for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, and for preventing, treating or ameliorating a medical condition, such as a disorder related to aberrant tubulin ligase activity, a disorder related to aberrant tubulin-carboxypeptidase activity, aberrant cellular proliferation, reproductive disorders, testicular disorders, testicular cancer, pulmonary disorders, lung cancer, gastrointestinal disorders, colon cancer, stomach cancer, neural disorders, brain cancer, liver cancer, or proliferative condition of the testis, lung, small intestine, brain or lymph tissue. The BGS-42 polypeptide, polynucleotide, or their modulators are also useful for treating infertility, Cushing's syndrome, emphysema, pneumonia, Addison's



CC disease, acromegaly, Alzheimer's disease, or Parkinson's disease. The BGS  
CC -42 polypeptide can be used as a preventive agent for immunological  
CC disorders including arthritis, asthma, AIDS, sepsis, acne, Sjogren's  
CC disease or scleroderma. The antibodies may be used to purify, detect and  
CC target the BGS-42 polypeptides. The present sequence is that of the  
CC tubulin tyrosine ligase protein consensus sequence which was used in the  
CC exemplification of the invention.

XX SQ Sequence 541 AA;

Query Match 95.0%; Score 514; DB 8; Length 541;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASSILKVVVSHQSCSRSSRSPROREAGSDDLSSRQDAENAEAKLGLPGQLVDIAC 60  
Db 1 MASSILKVVVSHQSCSRSSRSPROREAGSDDLSSRQDAENAEAKLGLPGQLVDIAC 60  
QY 61 KVCQAYLGQLEHEDIDTSADAVEDLTEAEWEDLTQYYSLVHGDAFISNSRNYFSQCAL 120  
Db 61 KVCQAYLGQLEHEDIDTSADAVEDLTEAEWEDLTQYYSLVHGDAFISNSRNYFSQCAL 120  
QY 121 LNRITSVNPOTIDGLRNIIWKPAKSGRDI VCMDRVVEILEAAADHPLSRNKVV 180  
Db 121 LNRITSVNPOTIDGLRNIIWKPAKSGRDI VCMDRVVEILEAAADHPLSRNKVV 180  
QY 181 QKIYETPLLCITKEDIQWFLVTDWNPITWIFKESYLRFTQRFSLDKLDSAIHLN 240  
Db 181 QKIYETPLLCITKEDIQWFLVTDWNPITWIFKESYLRFTQRFSLDKLDSAIHLN 240  
QY 241 AVQYKLVKNDVGRSPLPAHNMWTSRFBQYLRQGRGAVGWSVYPSMKKAIAHAMKVAQ 300  
Db 241 AVQYKLVKNDVGRSPLPAHNMWTSRFBQYLRQGRGAVGWSVYPSMKKAIAHAMKVAQ 300  
QY 301 DIVEPRKNSFELYGADFVLRGFRPWLIEINSPTWHPSTPTTAQLCAQVQEDTIKVAVD 360  
Db 301 DIVEPRKNSFELYGADFVLRGFRPWLIEINSPTWHPSTPTTAQLCAQVQEDTIKVAVD 360  
QY 361 RSCDIGNFELLNRQPVVEPPFSGSDLCVAGSVRRARQVLPVNCNKASASLLDAQPLK 420  
Db 361 RSCDIGNFELLNRQPVVEPPFSGSDLCVAGSVRRARQVLPVNCNKASASLLDAQPLK 420  
QY 421 ARGPSAMPDPAQPPSPALQDLGLKEEGLPLALLAPLRGAESGAAQPTRTKAAGKV 480  
Db 421 ARGPSAMPDPAQPPSPALQDLGLKEEGLPLALLAPLRGAESGAAQPTRTKAAGKV 480  
QY 481 ELFPACCRHVDSPAQNTGVPVPAQPAKSWDPNQLN 514  
Db 481 ELFPACCRHVDSPAQNTGVPVPAQPAKSWDPNQLN 514

RESULT 3  
ADJ93366  
ID ADJ93366 standard; protein; 293 AA.

AC ADJ93366;

XX 06-MAY-2004 (first entry)

DE Human BGS-42 protein-related TTL1 domain.

KW testis-specific tubulin tyrosine-ligase-like polypeptide;  
KW BGS-42 polypeptide; cytostatic; respiratory-gen; gastrointestinal-gen;  
KW neuroprotective; endocrine-gen; antiinflammatory; anabolic; hypertensive;  
KW osteopathic; nootropic; antiparkinsonian; antiarthritic; antiasthmatic;  
KW anti-HIV; antibacterial; immunosuppressive; antiseborrheic;  
KW dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;  
KW tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;  
KW testicular disorder; testicular cancer; pulmonary disorder; lung cancer;  
KW gastrointestinal disorder; colon cancer; stomach cancer; neural disorder;  
KW brain cancer; liver cancer; proliferative condition; testis; lung;  
KW small intestine; brain; lymph tissue; infertility; Cushing's syndrome;  
KW emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease;

KW Parkinson's disease; immunological disorder; arthritis; asthma; AIDS;  
KW sepsis; acne; Sjogren's disease; scleroderma; human; TTL1 domain.  
OS Homo sapiens.  
PN WO2004005487-A2.  
XX 15-JAN-2004.  
XX 09-JUL-2003; 2003WO-US021605.  
XX 09-JUL-2002; 2002US-0394725P.  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX Feder JN, Wu S, Nelson TC;  
XX WPI; 2004-099381/10.  
XX New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide,  
XX useful for preventing, treating or ameliorating a medical condition, e.g.  
XX aberrant cellular proliferation, reproductive disorders or testicular  
XX disorders.

PS Disclosure; SEQ ID NO 14; 343pp; English.

CC This invention relates to a novel testis-specific tubulin tyrosine-ligase  
CC -like polypeptide, designated the BGS-42 polypeptide. The invention may  
CC be useful for the development of compounds with a cytostatic, respiratory  
CC -Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen,  
CC antiinflammatory, anabolic, hypertensive, osteopathic, nootropic,  
CC antiparkinsonian, antiarthritic, antiasthmatic, anti-HIV, antibacterial,  
CC immunosuppressive, antiseborrheic or dermatological activity acting as  
CC tyrosine ligase modulators. In addition, the disclosed sequences may be  
CC useful for gene therapy. The BGS-42 polypeptide or polynucleotide can be  
CC used for diagnosing a pathological condition or a susceptibility to a  
CC pathological condition in a subject, and for preventing, treating or  
CC ameliorating a medical condition, such as a disorder related to aberrant  
CC tubulin ligase activity, a disorder related to aberrant tubulin-  
CC carboxypeptidase activity, aberrant cellular proliferation, reproductive  
CC disorders, testicular disorders, testicular cancer, pulmonary disorders,  
CC lung cancer, gastrointestinal disorders, colon cancer, stomach cancer,  
CC neural disorders, brain cancer, liver cancer, or proliferative condition  
CC of the testis, lung, small intestine, brain or lymph tissue. The BGS-42  
CC polypeptide, polynucleotide, or their modulators are also useful for  
CC treating infertility, Cushing's syndrome, emphysema, pneumonia, Addison's  
CC disease, acromegaly, Alzheimer's disease, or Parkinson's disease. The BGS  
CC -42 polypeptide can be used as a preventive agent for immunological  
CC disorders including arthritis, asthma, AIDS, sepsis, acne, Sjogren's  
CC disease or scleroderma. The antibodies may be used to purify, detect and  
CC target the BGS-42 polypeptides. The present sequence is that of the TTL1  
CC domain of the human BGS-42 protein of the invention.

XX Sequence 293 AA;

Query Match 54.2%; Score 293; DB 8; Length 293;  
Best Local Similarity 100.0%; Pred. No. 1.2e-307;  
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 EDITSDADAVEDLTEAEWEDLTQYYSLVHGDAFISNSRNYFSQCALNRTSVNPQTD 132  
Db 1 EDITSDADAVEDLTEAEWEDLTQYYSLVHGDAFISNSRNYFSQCALNRTSVNPQTD 60  
QY 133 IDGLRNIIWKPAKSGRDI VCMDRVVEILEAAADHPLSRNKVVQKIYETPLLCID 192  
Db 61 IDGLRNIIWKPAKSGRDI VCMDRVVEILEAAADHPLSRNKVVQKIYETPLLCID 120  
QY 193 TKFDIRQWFLVTDWNPITWIFKESYLRFTQRFSLDKLDSAIHLNNAVQYKLVKNDVGR 252  
Db 121 TKFDIRQWFLVTDWNPITWIFKESYLRFTQRFSLDKLDSAIHLNNAVQYKLVKNDVGR 180  
QY 253 SPILLPAHNMWTSRFBQYLRQGRGAVGWSVYPSMKKAIAHAMKVAQDHVPRKNSFEL 312

Db 181 SP LLPAHNNWMTSTRFOEYLQQRGAVGWSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL 240

QY 313 YGADFVLGRDRFWLIEINSSPTMHPSTPTVTAQLCAQVQEDTTIKVAVDRSCDI 365

Db 241 YGADFVLGRDRFWLIEINSSPTMHPSTPTVTAQLCAQVQEDTTIKVAVDRSCDI 293

RESULT 4

ADJ93360

ID ADJ93360 standard; protein; 242 AA.

XX

AC ADJ93360;

DT 06-MAY-2004 (first entry)

XX

DE Human BGS-42 protein sequence SeqID4.

XX

KW testis-specific tubulin tyrosine-ligase-like polypeptide;

KW BGS-42 polypeptide; cytosstatic; respiratory-Gen; gastrointestinal-Gen;

KW neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive;

KW osteopathic; nootropic; antiparkinsonian; antiarthritic; antiasthmatic;

KW anti-HIV; antibacterial; immunosuppressive; antiseborrheic;

KW dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;

KW tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;

KW testicular disorder; testicular cancer; pulmonary disorder; lung cancer;

KW gastrointestinal disorder; colon cancer; stomach cancer; neural disorder;

KW brain cancer; liver cancer; proliferative condition; testis; lung;

KW small intestine; brain; lymph tissue; infertility; Cushing's syndrome;

KW emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease;

KW Parkinson's disease; immunological disorder; arthritis; asthma; AIDS;

KW sepsis; acne; Sjogren's disease; scleroderma; human.

XX

OS Homo sapiens.

XX

PN WO2004005487-A2.

XX

PD 15-JAN-2004.

XX

PF 09-JUL-2003; 2003WO-US021605.

XX

PR 09-JUL-2002; 2002US-0394725P.

XX

PA (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX

PI Feder JN, Wu S, Nelson TC;

XX

DR WPI; 2004-099381/10.

XX

XX

PT New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide,

PT useful for preventing, treating or ameliorating a medical condition, e.g.

PT aberrant cellular proliferation, reproductive disorders or testicular

PT disorders.

XX

XX

PS Disclosure; SEQ ID NO 4; 343pp; English.

XX

CC This invention relates to a novel testis-specific tubulin tyrosine-ligase

CC -like polypeptide, designated the BGS-42 polypeptide. The invention may

CC be useful for the development of compounds with a cytosstatic, respiratory

CC -Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen,

CC antiinflammatory, anabolic, hypertensive, osteopathic, nootropic,

CC antiparkinsonian, antiarthritic, antiasthmatic, anti-HIV, antibacterial,

CC immunosuppressive, antiseborrheic or dermatological activity acting as

CC tyrosine ligase modulators. In addition, the disclosed sequences may be

CC useful for gene therapy. The BGS-42 polypeptide or polynucleotide can be

CC used for diagnosing a pathological condition or a susceptibility to a

CC pathological condition in a subject, and for preventing, treating or

CC ameliorating a medical condition, such as a disorder related to aberrant

CC tubulin ligase activity, a disorder related to aberrant tubulin-

CC carboxypeptidase activity, aberrant cellular proliferation, reproductive

CC disorders, testicular disorders, testicular cancer, pulmonary disorders,

CC lung cancer, gastrointestinal disorders, colon cancer, stomach cancer,

CC neural disorders, brain cancer, liver cancer, or proliferative condition

CC of the testis, lung, small intestine, brain or lymph tissue. The BGS-42

CC polypeptide, polynucleotide, or their modulators are also useful for

CC treating infertility, Cushing's syndrome, emphysema, pneumonia, Addison's

CC disease, acromegaly, Alzheimer's disease, or Parkinson's disease. The BGS

CC -42 polypeptide can be used as a preventive agent for immunological

CC disorders including arthritis, asthma, AIDS, sepsis, acne, Sjogren's

CC disease or scleroderma. The antibodies may be used to purify, detect and

CC target the BGS-42 polypeptides. The present sequence is that of the human

CC BGS-42 protein (partial sequence) of the invention.

XX

XX

SQ Sequence 242 AA;

Query Match 44.7%; Score 242; DB 8; Length 242;

Best Local Similarity 100.0%; Pred. No. 1.7e-252;

Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 IDGLRNIWIIPAAKSRGRDIVCMRDRVEIELEAAADHPLSRDNKVVQKYIETPLLICD 192

Db 1 IDGLRNIWIIPAAKSRGRDIVCMRDRVEIELEAAADHPLSRDNKVVQKYIETPLLICD 60

QY 193 TKFDIRQWFLVTDWNP LTTTFYKESYLRFSTQRFSLDKLDSAIHLGNNAVQKYLKNDVGR 252

Db 61 TKFDIRQWFLVTDWNP LTTTFYKESYLRFSTQRFSLDKLDSAIHLGNNAVQKYLKNDVGR 120

QY 253 SP LLPAHNNWMTSTRFOEYLQQRGAVGWSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL 312

Db 121 SP LLPAHNNWMTSTRFOEYLQQRGAVGWSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL 180

QY 313 YGADFVLGRDRFWLIEINSSPTMHPSTPTVTAQLCAQVQEDTTIKVAVDRSCDIGNFELLW 372

Db 181 YGADFVLGRDRFWLIEINSSPTMHPSTPTVTAQLCAQVQEDTTIKVAVDRSCDIGNFELLW 240

QY 373 RQ 374

Db 241 RQ 242

RESULT 5

ADU02747

ID ADU02747 standard; protein; 402 AA.

XX

AC ADU02747;

XX

DT 27-JAN-2005 (first entry)

XX

DE Novel human polypeptide seqid 1214.

XX

KW cytosstatic; antipsoriatic; antiinflammatory; gene therapy; Nanodisc;

KW proliferative disorder; inflammatory disorder; immune disorder;

KW metabolic disorder; bone disorder; CNS disorder; cancer; psoriasis;

KW ulcerative colitis; human.

XX

OS Homo sapiens.

XX

PN WO2004093804-A2.

XX

PD 04-NOV-2004.

XX

PF 19-APR-2004; 2004WO-US012047.

XX

PR 18-APR-2003; 2003US-0463708P.

PR 18-APR-2003; 2003US-0463732P.

PR 02-MAY-2003; 2003US-0467199P.

PR 02-MAY-2003; 2003US-0467230P.

PR 19-MAY-2003; 2003US-0471306P.

PR 19-MAY-2003; 2003US-0471336P.

PR 08-JUL-2003; 2003US-0485223P.

PR 08-JUL-2003; 2003US-0485224P.

PR 14-JUL-2003; 2003US-0486446P.

PR 14-JUL-2003; 2003US-0486480P.

PR 08-AUG-2003; 2003US-0493573P.

PR 08-AUG-2003; 2003US-0493577P.

PR 08-SEP-2003; 2003US-0505059P.

XX



CC target the BGS-42 polypeptides. The present sequence is that of a peptide  
 CC fragment of the human BGS-42 protein of the invention.

XX Sequence 49 AA;

Query Match 9.1%; Score 49; DB 8; Length 49;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-44;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 DTKFDIRQWFLVTDWNPNTIWFYKESYLRFSTQRFSLDKLDSAIHLCNN 240

Db 1 DTKFDIRQWFLVTDWNPNTIWFYKESYLRFSTQRFSLDKLDSAIHLCNN 49

RESULT 7

ADJ93376

ID ADJ93376 standard; peptide; 42 AA.

AC ADJ93376;

DT 06-MAY-2004 (first entry)

XX Human BGS-42 protein peptide fragment SegID24.

XX testis-specific tubulin tyrosine-ligase-like polypeptide;  
 KW BGS-42 polypeptide; cytosolic; respiratory-Gen; gastrointestinal-Gen;  
 KW neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive;  
 KW osteopathic; nontropic; antiparkinsonian; antiarthritic; antiasthmatic;  
 KW anti-HIV; antibacterial; immunosuppressive; antiseborrheic;  
 KW dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;  
 KW tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;  
 KW testicular disorder; testicular cancer; pulmonary disorder; lung cancer;  
 KW gastrointestinal disorder; colon cancer; stomach cancer; neural disorder;  
 KW brain cancer; liver cancer; proliferative condition; testis; lung;  
 KW small intestine; brain; lymph tissue; infertility; Cushing's syndrome;  
 KW emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease;  
 KW Parkinson's disease; immunological disorder; arthritis; asthma; AIDS;  
 KW sepsis; acne; Sjogren's disease; scleroderma; human.

XX Homo sapiens.

PN WO2004005487-A2.

PD 15-JAN-2004.

XX 09-JUL-2003; 2003WO-US021605.

XX 09-JUL-2002; 2002US-0394725P.

XX (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX Feder JN, Wu S, Nelson TC;

XX WPI; 2004-099381/10.

XX New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide,  
 PT useful for preventing, treating or ameliorating a medical condition, e.g.  
 PT aberrant cellular proliferation, reproductive disorders or testicular  
 disorders.

XX Disclosure; SEQ ID NO 24; 343pp; English.

XX This invention relates to a novel testis-specific tubulin tyrosine-ligase  
 CC -like polypeptide, designated the BGS-42 polypeptide. The invention may  
 CC be useful for the development of compounds with a cytosolic, respiratory  
 CC -Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen,  
 CC antiinflammatory, anabolic, hypertensive, osteopathic, nontropic,  
 CC antiparkinsonian, antiarthritic, antiasthmatic, anti-HIV, antibacterial,  
 CC immunosuppressive, antiseborrheic or dermatological activity acting as,  
 CC tyrosine ligase modulators. In addition, the disclosed sequences may be  
 CC useful for gene therapy. The BGS-42 polypeptide or polynucleotide can be  
 CC used for diagnosing a pathological condition or a susceptibility to a  
 CC pathological condition in a subject, and for preventing, treating or

CC ameliorating a medical condition, such as a disorder related to aberrant  
 CC tubulin ligase activity, a disorder related to aberrant tubulin-  
 CC carboxypeptidase activity, aberrant cellular proliferation, reproductive  
 CC disorders, testicular disorders, testicular cancer, pulmonary disorders,  
 CC lung cancer, gastrointestinal disorders, colon cancer, stomach cancer,  
 CC neural disorders, brain cancer, liver cancer, or proliferative condition  
 CC of the testis, lung, small intestine, brain or lymph tissue. The BGS-42  
 CC polypeptide, polynucleotide, or their modulators are also useful for  
 CC treating infertility, Cushing's syndrome, emphysema, pneumonia, Addison's  
 CC disease, acromegaly, Alzheimer's disease, or Parkinson's disease. The BGS  
 CC -42 polypeptide can be used as a preventive agent for immunological  
 CC disorders including arthritis, asthma, AIDS, sepsis, acne, Sjogren's  
 CC disease or scleroderma. The antibodies may be used to purify, detect and  
 CC target the BGS-42 polypeptides. The present sequence is that of a peptide  
 CC fragment of the human BGS-42 protein of the invention.

XX Sequence 42 AA;

Query Match 7.8%; Score 42; DB 8; Length 42;  
 Best Local Similarity 100.0%; Pred. No. 1e-36;  
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 482 LPACPCRHVDSQAPNTGVFVAQPAKSWDPNQLNAHPLEPVL 523

Db 1 LPACPCRHVDSQAPNTGVFVAQPAKSWDPNQLNAHPLEPVL 42

RESULT 8

ADJ93452

ID ADJ93452 standard; protein; 61 AA.

AC ADJ93452;

XX 06-MAY-2004 (first entry)

XX Human BGS-42 protein-related protein sequence #103.

XX testis-specific tubulin tyrosine-ligase-like polypeptide;  
 KW BGS-42 polypeptide; cytosolic; respiratory-Gen; gastrointestinal-Gen;  
 KW neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive;  
 KW osteopathic; nontropic; antiparkinsonian; antiarthritic; antiasthmatic;  
 KW anti-HIV; antibacterial; immunosuppressive; antiseborrheic;  
 KW dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;  
 KW tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;  
 KW testicular disorder; testicular cancer; pulmonary disorder; lung cancer;  
 KW gastrointestinal disorder; colon cancer; stomach cancer; neural disorder;  
 KW brain cancer; liver cancer; proliferative condition; testis; lung;  
 KW small intestine; brain; lymph tissue; infertility; Cushing's syndrome;  
 KW emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease;  
 KW Parkinson's disease; immunological disorder; arthritis; asthma; AIDS;  
 KW sepsis; acne; Sjogren's disease; scleroderma; human.

XX Homo sapiens.

XX WO2004005487-A2.

XX 15-JAN-2004.

XX 09-JUL-2003; 2003WO-US021605.

XX 09-JUL-2002; 2002US-0394725P.

XX (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX Feder JN, Wu S, Nelson TC;

XX WPI; 2004-099381/10.

XX New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide,  
 PT useful for preventing, treating or ameliorating a medical condition, e.g.  
 PT aberrant cellular proliferation, reproductive disorders or testicular  
 PT disorders.

PS Disclosure; Fig 7B; 343pp; English.

XX This invention relates to a novel testis-specific tubulin tyrosine-ligase

XX -like polypeptide, designated the BGS-42 polypeptide. The invention may

CC be useful for the development of compounds with a cytostatic, respiratory

CC -Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen,

CC antiparkinsonian, antiarthritic, antiaslathmatic, nootropic,

CC immunosuppressive, antiseborrheic or dermatological activity acting as

CC tyrosine ligase modulators. In addition, the disclosed sequences may be

CC used for gene therapy. The BGS-42 polypeptide or polynucleotide can be

CC used for diagnosing a pathological condition or a susceptibility to a

CC pathological condition in a subject, and for preventing, treating or

CC ameliorating a medical condition, such as a disorder related to aberrant

CC tubulin ligase activity, a disorder related to aberrant tubulin-

CC carboxypeptidase activity, aberrant cellular proliferation, reproductive

CC disorders, testicular disorders, testicular cancer, pulmonary disorders,

CC lung cancer, gastrointestinal disorders, colon cancer, stomach cancer,

CC neural disorders, brain cancer, liver cancer, or proliferative condition

CC of the testis, lung, small intestine, brain or lymph tissue. The BGS-42

CC polypeptide, polynucleotide, or their modulators are also useful for

CC treating infertility, Cushing's syndrome, emphysema, pneumonia, Addison's

CC disease, acromegaly, Alzheimer's disease, or Parkinson's disease. The BGS

CC -42 polypeptide can be used as a preventive agent for immunological

CC disorders including arthritis, asthma, AIDS, sepsis, acne, Sjogren's

CC disease or scleroderma. The antibodies may be used to purify, detect and

CC target the BGS-42 polypeptides. The present sequence is that of a protein

CC related to the human BGS-42 protein of the invention.

XX Sequence 61 AA;

SQ

Query Match 7.2%; Score 39; DB 8; Length 61;

Best Local Similarity 100.0%; Pred. No. 2.6e-33;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASSILKWVSHQSCSRSSRPRDQREBAGSSDLSRQ 39

DB 1 MASSILKWVSHQSCSRSSRPRDQREBAGSSDLSRQ 39

RESULT 9

ADJ93374

ID ADJ93374 standard; peptide; 26 AA.

XX

AC ADJ93374;

XX

DT 06-MAY-2004 (first entry)

XX

DE Human BGS-42 protein peptide fragment SeqID22.

XX

KW testis-specific tubulin tyrosine-ligase-like polypeptide;

KW BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;

KW neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive;

KW osteopathic; nootropic; antiparkinsonian; antiarthritic; antiaslathmatic;

KW anti-HIV; antibacterial; immunosuppressive; antiseborrheic;

KW dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;

KW tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;

KW testicular disorder; testicular cancer; pulmonary disorder; lung cancer;

KW gastrointestinal disorder; colon cancer; stomach cancer; neural disorder;

KW brain cancer; liver cancer; proliferative condition; testis; lung;

KW small intestine; brain; lymph tissue; infertility; Cushing's syndrome;

KW emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease;

KW Parkinson's disease; immunological disorder; arthritis; asthma; AIDS;

KW sepsis; acne; Sjogren's disease; scleroderma; human.

XX Homo sapiens.

OS

XX WO2004005487-A2.

PN

XX 15-JAN-2004.

PD

XX 09-JUL-2003; 2003WO-US021605.

PF

XX

09-JUL-2002; 2002US-0394725P.

(BRIM ) BRISTOL-MYERS SQUIBB CO.

Feder JN, Wu S, Nelson TC;

WPI; 2004-099381/10.

New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide,

useful for preventing, treating or ameliorating a medical condition, e.g.

aberrant cellular proliferation, reproductive disorders or testicular

disorders.

Disclosure; SEQ ID NO 22; 343pp; English.

This invention relates to a novel testis-specific tubulin tyrosine-ligase

-like polypeptide, designated the BGS-42 polypeptide. The invention may

be useful for the development of compounds with a cytostatic, respiratory

-Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen,

antiparkinsonian, antiarthritic, antiaslathmatic, nootropic,

immunosuppressive, antiseborrheic or dermatological activity acting as

tyrosine ligase modulators. In addition, the disclosed sequences may be

used for gene therapy. The BGS-42 polypeptide or polynucleotide can be

used for diagnosing a pathological condition or a susceptibility to a

pathological condition in a subject, and for preventing, treating or

ameliorating a medical condition, such as a disorder related to aberrant

tubulin ligase activity, a disorder related to aberrant tubulin-

carboxypeptidase activity, aberrant cellular proliferation, reproductive

disorders, testicular disorders, testicular cancer, pulmonary disorders,

lung cancer, gastrointestinal disorders, colon cancer, stomach cancer,

neural disorders, brain cancer, liver cancer, or proliferative condition

of the testis, lung, small intestine, brain or lymph tissue. The BGS-42

polypeptide, polynucleotide, or their modulators are also useful for

treating infertility, Cushing's syndrome, emphysema, pneumonia, Addison's

disease, acromegaly, Alzheimer's disease, or Parkinson's disease. The BGS

-42 polypeptide can be used as a preventive agent for immunological

disorders including arthritis, asthma, AIDS, sepsis, acne, Sjogren's

disease or scleroderma. The antibodies may be used to purify, detect and

target the BGS-42 polypeptides. The present sequence is that of a peptide

fragment of the human BGS-42 protein of the invention.

Sequence 26 AA;

Query Match 4.8%; Score 26; DB 8; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.4e-19;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 332 SSPTMHPSTPVTQAQLCAQVQEDTIKV 357

DB 1 SSPTMHPSTPVTQAQLCAQVQEDTIKV 26

RESULT 10

ADJ93371

ID ADJ93371 standard; peptide; 23 AA.

XX

AC ADJ93371;

XX

DT 06-MAY-2004 (first entry)

XX

DE Human BGS-42 protein peptide fragment SeqID19.

XX

KW testis-specific tubulin tyrosine-ligase-like polypeptide;

KW BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;

KW neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive;

KW osteopathic; nootropic; antiparkinsonian; antiarthritic; antiaslathmatic;

KW anti-HIV; antibacterial; immunosuppressive; antiseborrheic;

KW dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;

KW tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;

KW testicular disorder; testicular cancer; pulmonary disorder; lung cancer;

KW gastrointestinal disorder; colon cancer; stomach cancer; neural disorder;

KW brain cancer; liver cancer; proliferative condition; testis; lung;



QY 525 LKTAEGALRPPPGGKGS 541  
 Db 1 LKTAEGALRPPPGGKGS 17  
 RESULT 12  
 ADJ93397  
 ID ADJ93397 standard; peptide; 16 AA.  
 XX  
 AC ADJ93397;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Human BGS-42 protein-related N-myristoylation peptide SeqID47.  
 XX  
 KW testis-specific tubulin tyrosine-ligase-like polypeptide;  
 KW BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;  
 KW neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive;  
 KW osteopathic; nontropic; antiparkinsonian; antiarthritic; antiasthmatic;  
 KW anti-HIV; antibacterial; immunosuppressive; antiseborrheic;  
 KW dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;  
 KW tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;  
 KW testicular disorder; testicular cancer; pulmonary disorder; lung cancer;  
 KW gastrointestinal disorder; colon cancer; stomach cancer; neural disorder;  
 KW brain cancer; liver cancer; proliferative condition; testis; lung;  
 KW small intestine; brain; lymph tissue; infertility; Cushing's syndrome;  
 KW emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease;  
 KW Parkinson's disease; immunological disorder; arthritis; asthma; AIDS;  
 KW sepsis; acne; Sjogren's disease; scleroderma; human; N-myristoylation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004005487-A2.  
 XX  
 XX 15-JAN-2004.  
 XX  
 PF 09-JUL-2003; 2003WO-US021605.  
 XX  
 XX 09-JUL-2002; 2002US-0394725P.  
 PR  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX  
 PI Feder JN, Wu S, Nelson TC;  
 XX  
 XX WPI; 2004-099381/10.  
 XX  
 PT New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide,  
 PT useful for preventing, treating or ameliorating a medical condition, e.g.  
 PT aberrant cellular proliferation, reproductive disorders or testicular  
 disorders.  
 XX  
 PS Disclosure; SEQ ID NO 47; 343pp; English.  
 XX  
 CC This invention relates to a novel testis-specific tubulin tyrosine-ligase  
 CC -like polypeptide, designated the BGS-42 polypeptide. The invention may  
 CC be useful for the development of compounds with a cytostatic, respiratory  
 CC -Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen,  
 CC antiinflammatory, anabolic, hypertensive, osteopathic, nontropic,  
 CC antiparkinsonian, antiarthritic, antiasthmatic, anti-HIV, antibacterial,  
 CC immunosuppressive, antiseborrheic or dermatological activity acting as  
 CC tyrosine ligase modulators. In addition, the disclosed sequences may be  
 CC useful for gene therapy. The BGS-42 polypeptide or polynucleotide can be  
 CC used for diagnosing a pathological condition or a susceptibility to a  
 CC pathological condition in a subject, and for preventing, treating or  
 CC ameliorating a medical condition, such as a disorder related to aberrant  
 CC tubulin ligase activity, a disorder related to aberrant tubulin-  
 CC carboxypeptidase activity, aberrant cellular proliferation, reproductive  
 CC disorders, testicular disorders, testicular cancer, pulmonary disorders,  
 CC lung cancer, gastrointestinal disorders, colon cancer, stomach cancer,  
 CC neural disorders, brain cancer, liver cancer, or proliferative condition  
 CC of the testis, lung, small intestine, brain or lymph tissue. The BGS-42  
 CC polypeptide, polynucleotide, or their modulators are also useful for

CC treating infertility, Cushing's syndrome, emphysema, pneumonia, Addison's  
 CC disease, acromegaly, Alzheimer's disease, or Parkinson's disease. The BGS  
 CC -42 polypeptide can be used as a preventive agent for immunological  
 CC disorders including arthritis, asthma, AIDS, sepsis, acne, Sjogren's  
 CC disease or scleroderma. The antibodies may be used to purify, detect and  
 CC target the BGS-42 polypeptides. The present sequence is that of a peptide  
 CC which represents a site of N-myristoylation in the human BGS-42 protein  
 CC of the invention.  
 XX  
 SQ Sequence 16 AA;  
 Query Match 3.0%; Score 16; DB 8; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-09;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 379 PPPFGSGLCVAGSV 394  
 Db 1 PPPFGSGLCVAGSV 16  
 RESULT 13  
 ADJ93398  
 ID ADJ93398 standard; peptide; 16 AA.  
 XX  
 AC ADJ93398;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Human BGS-42 protein-related N-myristoylation peptide SeqID48.  
 XX  
 KW testis-specific tubulin tyrosine-ligase-like polypeptide;  
 KW BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;  
 KW neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive;  
 KW osteopathic; nontropic; antiparkinsonian; antiarthritic; antiasthmatic;  
 KW anti-HIV; antibacterial; immunosuppressive; antiseborrheic;  
 KW dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;  
 KW tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;  
 KW testicular disorder; testicular cancer; pulmonary disorder; lung cancer;  
 KW gastrointestinal disorder; colon cancer; stomach cancer; neural disorder;  
 KW brain cancer; liver cancer; proliferative condition; testis; lung;  
 KW small intestine; brain; lymph tissue; infertility; Cushing's syndrome;  
 KW emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease;  
 KW Parkinson's disease; immunological disorder; arthritis; asthma; AIDS;  
 KW sepsis; acne; Sjogren's disease; scleroderma; human; N-myristoylation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004005487-A2.  
 XX  
 XX 15-JAN-2004.  
 XX  
 PF 09-JUL-2003; 2003WO-US021605.  
 XX  
 XX 09-JUL-2002; 2002US-0394725P.  
 PR  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX  
 PI Feder JN, Wu S, Nelson TC;  
 XX  
 XX WPI; 2004-099381/10.  
 XX  
 PT New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide,  
 PT useful for preventing, treating or ameliorating a medical condition, e.g.  
 PT aberrant cellular proliferation, reproductive disorders or testicular  
 disorders.  
 XX  
 PS Disclosure; SEQ ID NO 48; 343pp; English.  
 XX  
 CC This invention relates to a novel testis-specific tubulin tyrosine-ligase  
 CC -like polypeptide, designated the BGS-42 polypeptide. The invention may  
 CC be useful for the development of compounds with a cytostatic, respiratory  
 CC -Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen,  
 CC antiinflammatory, anabolic, hypertensive, osteopathic, nontropic,  
 CC antiparkinsonian, antiarthritic, antiasthmatic, anti-HIV, antibacterial,  
 CC immunosuppressive, antiseborrheic or dermatological activity acting as  
 CC tyrosine ligase modulators. In addition, the disclosed sequences may be  
 CC useful for gene therapy. The BGS-42 polypeptide or polynucleotide can be  
 CC used for diagnosing a pathological condition or a susceptibility to a  
 CC pathological condition in a subject, and for preventing, treating or  
 CC ameliorating a medical condition, such as a disorder related to aberrant  
 CC tubulin ligase activity, a disorder related to aberrant tubulin-  
 CC carboxypeptidase activity, aberrant cellular proliferation, reproductive  
 CC disorders, testicular disorders, testicular cancer, pulmonary disorders,  
 CC lung cancer, gastrointestinal disorders, colon cancer, stomach cancer,  
 CC neural disorders, brain cancer, liver cancer, or proliferative condition  
 CC of the testis, lung, small intestine, brain or lymph tissue. The BGS-42  
 CC polypeptide, polynucleotide, or their modulators are also useful for



CC antiparkinsonian, antiarthritic, antiasthmatic, anti-HIV, antibacterial,  
 CC immunosuppressive, antiseborrheic or dermatological activity acting as  
 CC tyrosine ligase modulators. In addition, the disclosed sequences may be  
 CC useful for gene therapy. The BGS-42 polypeptide or polynucleotide can be  
 CC used for diagnosing a pathological condition or a susceptibility to a  
 CC pathological condition in a subject, and for preventing, treating or  
 CC ameliorating a medical condition, such as a disorder related to aberrant  
 CC tubulin ligase activity, a disorder related to aberrant tubulin-  
 CC carboxypeptidase activity, aberrant cellular proliferation, reproductive  
 CC disorders, testicular disorders, testicular cancer, pulmonary disorders,  
 CC lung cancer, gastrointestinal disorders, colon cancer, stomach cancer,  
 CC neural disorders, brain cancer, liver cancer, or proliferative condition  
 CC of the testis, lung, small intestine, brain or lymph tissue. The BGS-42  
 CC polypeptide, polynucleotide, or their modulators are also useful for  
 CC treating infertility, Cushing's syndrome, emphysema, pneumonia, Addison's  
 CC disease, acromegaly, Alzheimer's disease, or Parkinson's disease. The BGS  
 CC -42 polypeptide can be used as a preventive agent for immunological  
 CC disorders including arthritis, asthma, AIDS, sepsis, acne, Sjogren's  
 CC disease or scleroderma. The antibodies may be used to purify, detect and  
 CC target the BGS-42 polypeptides. The present sequence is that of a peptide  
 CC of the invention.  
 CC  
 XX SQ Sequence 16 AA;

Query Match 3.0%; Score 16; DB 8; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-09;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 445 LKEEGLPLALLAPLR 460  
 Db 1 LKEEGLPLALLAPLR 16  
 |||||

## RESULT 14

ADJ93401  
 ID ADJ93401 standard; peptide; 16 AA.

XX AC ADJ93401;

XX DT 06-MAY-2004 (first entry)

XX DE Human BGS-42 protein-related N-myristoylation peptide SeqID51.

XX testis-specific tubulin tyrosine-ligase-like polypeptide;  
 KW BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;  
 KW neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive;  
 KW osteopathic; nontropic; antiparkinsonian; antiarthritic; antiasthmatic;  
 KW anti-HIV; antibacterial; immunosuppressive; antiseborrheic;  
 KW dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;  
 KW tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;  
 KW testicular disorder; testicular cancer; pulmonary disorder; lung cancer;  
 KW gastrointestinal disorder; colon cancer; stomach cancer; neural disorder;  
 KW brain cancer; liver cancer; proliferative condition; testis; lung;  
 KW small intestine; brain; lymph tissue; infertility; Cushing's syndrome;  
 KW emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease;  
 KW Parkinson's disease; immunological disorder; arthritis; aschma; AIDS;  
 KW sepsis; acne; Sjogren's disease; scleroderma; human; N-myristoylation.

XX OS Homo sapiens.

XX PN W02004005487-A2.

XX PD 15-JAN-2004.

XX PF 09-JUL-2003; 2003WO-US021605.

XX PR 09-JUL-2002; 2002US-0394725P.

XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX PI Feder JN, Wu S, Nelson TC;

XX

DR WPI; 2004-099381/10.

XX New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide,  
 PT useful for preventing, treating or ameliorating a medical condition, e.g.  
 PT aberrant cellular proliferation, reproductive disorders or testicular  
 PT disorders.

XX Disclosure; SEQ ID NO 51; 343pp; English.

XX This invention relates to a novel testis-specific tubulin tyrosine-ligase  
 CC -like polypeptide, designated the BGS-42 polypeptide. The invention may  
 CC be useful for the development of compounds with a cytostatic, respiratory  
 CC -Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen,  
 CC antiinflammatory, anabolic, hypertensive, osteopathic, nontropic,  
 CC antiparkinsonian, antiarthritic, antiasthmatic, anti-HIV, antibacterial,  
 CC immunosuppressive, antiseborrheic or dermatological activity acting as  
 CC tyrosine ligase modulators. In addition, the disclosed sequences may be  
 CC useful for gene therapy. The BGS-42 polypeptide or polynucleotide can be  
 CC used for diagnosing a pathological condition or a susceptibility to a  
 CC pathological condition in a subject, and for preventing, treating or  
 CC ameliorating a medical condition, such as a disorder related to aberrant  
 CC tubulin ligase activity, a disorder related to aberrant tubulin-  
 CC carboxypeptidase activity, aberrant cellular proliferation, reproductive  
 CC disorders, testicular disorders, testicular cancer, pulmonary disorders,  
 CC lung cancer, gastrointestinal disorders, colon cancer, stomach cancer,  
 CC neural disorders, brain cancer, liver cancer, or proliferative condition  
 CC of the testis, lung, small intestine, brain or lymph tissue. The BGS-42  
 CC polypeptide, polynucleotide, or their modulators are also useful for  
 CC treating infertility, Cushing's syndrome, emphysema, pneumonia, Addison's  
 CC disease, acromegaly, Alzheimer's disease, or Parkinson's disease. The BGS  
 CC -42 polypeptide can be used as a preventive agent for immunological  
 CC disorders including arthritis, asthma, AIDS, sepsis, acne, Sjogren's  
 CC disease or scleroderma. The antibodies may be used to purify, detect and  
 CC target the BGS-42 polypeptides. The present sequence is that of a peptide  
 CC of the invention.  
 CC  
 XX SQ Sequence 16 AA;

Query Match 3.0%; Score 16; DB 8; Length 16;

Best Local Similarity 100.0%; Pred. No. 5.8e-09;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 519 EPVIRGLKTAEGALRP 534

Db 1 EPVIRGLKTAEGALRP 16  
 |||||

## RESULT 15

ADJ93396

ID ADJ93396 standard; peptide; 16 AA.

XX AC ADJ93396;

XX DT 06-MAY-2004 (first entry)

XX DE Human BGS-42 protein-related N-myristoylation peptide SeqID46.

XX testis-specific tubulin tyrosine-ligase-like polypeptide;  
 KW BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;  
 KW neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive;  
 KW osteopathic; nontropic; antiparkinsonian; antiarthritic; antiasthmatic;  
 KW anti-HIV; antibacterial; immunosuppressive; antiseborrheic;  
 KW dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;  
 KW tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;  
 KW testicular disorder; testicular cancer; pulmonary disorder; lung cancer;  
 KW gastrointestinal disorder; colon cancer; stomach cancer; neural disorder;  
 KW brain cancer; liver cancer; proliferative condition; testis; lung;  
 KW small intestine; brain; lymph tissue; infertility; Cushing's syndrome;  
 KW emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease;  
 KW Parkinson's disease; immunological disorder; arthritis; aschma; AIDS;  
 KW sepsis; acne; Sjogren's disease; scleroderma; human; N-myristoylation.



OS Homo sapiens.  
XX WO2004005487-A2.  
PN  
XX  
XX  
PD 15-JAN-2004.  
XX  
XX 09-JUL-2003; 2003WO-US021605.  
XX  
XX PF  
XX PR  
XX 09-JUL-2002; 2002US-0394725P.  
XX  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
PA  
XX Feder JN, Wu S, Nelson TC;  
PI  
XX WPI; 2004-099381/10.  
XX  
XX New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide,  
PT useful for preventing, treating or ameliorating a medical condition, e.g.  
PT aberrant cellular proliferation, reproductive disorders or testicular  
PT disorders.  
XX  
XX Disclosure; SEQ ID NO 46; 343pp; English.  
PS  
XX  
XX CC This invention relates to a novel testis-specific tubulin tyrosine-ligase  
CC -like polypeptide, designated the BGS-42 polypeptide. The invention may  
CC be useful for the development of compounds with a cytostatic, respiratory  
CC -Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen, respiratory  
CC antiinflammatory, anabolic, hypertensive, osteopathic, nootropic,  
CC antiparkinsonian, antiarthritic, antiasthmatic, anti-HIV, antibacterial,  
CC immunosuppressive, antiseborrheic or dermatological activity acting as  
CC tyrosine ligase modulators. In addition, the disclosed sequences may be  
CC useful for gene therapy. The BGS-42 polypeptide or polynucleotide can be  
CC used for diagnosing a pathological condition or a susceptibility to a  
CC pathological condition in a subject, and for preventing, treating or  
CC ameliorating a medical condition, such as a disorder related to aberrant  
CC tubulin ligase activity, a disorder related to aberrant tubulin-  
CC carboxypeptidase activity, aberrant cellular proliferation, reproductive  
CC disorders, testicular disorders, testicular cancer, pulmonary disorders,  
CC lung cancer, gastrointestinal disorders, colon cancer, stomach cancer,  
CC neural disorders, brain cancer, liver cancer, or proliferative condition  
CC of the testis, lung, small intestine, brain or lymph tissue. The BGS-42  
CC polypeptide, polynucleotide, or their modulators are also useful for  
CC treating infertility, Cushing's syndrome, emphysema, pneumonia, Addison's  
CC disease, acromegaly, Alzheimer's disease, or Parkinson's disease. The BGS  
CC -42 polypeptide can be used as a preventive agent for immunological  
CC disorders including arthritis, asthma, AIDS, sepsis, acne, Sjogren's  
CC disease or scleroderma. The antibodies may be used to purify, detect and  
CC target the BGS-42 polypeptides. The present sequence is that of a peptide  
CC which represents a site of N-myristoylation in the human BGS-42 protein  
CC of the invention.  
XX  
XX SQ Sequence 16 AA;

Query Match 3.0%; Score 16; DB 8; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.8e-09;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 QRQGRGAVWGSVITYPS 287  
DB 1 QRQGRGAVWGSVITYPS 16

Search completed: May 15, 2006, 09:57:38  
Job time : 63 secs

**THIS PAGE BLANK (USPTO)**